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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries GenEmb1:* Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	DEFINITION		C.glutamicum x96471	cum Lysk	and	a lyst genes.		
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		Bac	teria;	Bacteria, Actinobacteria,	act.	teria, Actinobacteridae,	teridae; Actinomycetales;	
	REFERENCE		Inchac	30311773	•	or y menacces tack		
	AUTHORS		Vrlin M	Sahm H		and Eggeling.L.		

AUTHORS TITLE

 ${\tt Vrljic}, M.$, Sahm, H. and Bggeling, L. A new type of cellular function: A new type of transporter with a new type of cellular function:

DOUGNAL STATES AFORT from Corynabacterium glutamicum PRESENSENCE 2. (bases 1 to 2334) ANTHONS 21706 PRESENSENCE 2. (bases 1 to 2334) ANTHONS 21716 PRESENCE 2. (bases 1 to 2334) ANTHONS 21716 PRESENCE 2. (bases 1 to 2334) PRESENCE 2. (bases 2 to 2334) PRESENCE 2. (bases		ACGGTCTTGAAGCAATCTTTGGAACCGAAGGTAGACCATCAACGGCCCAATCTAGAACTTCTAGAACCGAACCAACAACAACAACAACAACAACAACAACAA	601 GAGCGTTGCTCCACCCCAAGAAGCTACCTCGTTGAACACGGGGAAACCATGTGGATAG 660 601 GAGCGTTGCTCCACCCCAAGAAGCTACCTCGTTGAACACGGGGAAACCATGTGGATAG 660 601 GAATCTGCTGATGGCGATGGTTAACGGGATTTCAGCAAGGGGAAACCATGTGGGC 720 601 CGAATCTGCTTGATGGCGATGGTTAACGGGATTTCAGCAAGGGGTCCAGATAGTTGCGC 720 721 TTTAGTTTCTGCTTGATGGCGATAGTTAACGGGATTTCAGCAAGGGTTCACCCGC 780 721 TTTAGTTTCTGCTTGCTGAACACCCATTTCCGCGCTGCTTGCACAAGAACTTCACCCGC 780 721 TTTAGTTTCTGCTTGCAACACACACATTTCCGCGCTGCTTGCACAAGAACTTCACCCGC 780 722 TTTAGTTTCTGCTTGCAAGACAACACCATTTTCCGCGCTGCTTGCACAAGAACTTCACCCGC 780 723 TTTAGTTTCTGCTTGCAAGACACACATTTTCCGCGCTGCTTTGCACAAGACTTCACCCGC 780 724 TTTAGTTTCTGCTTGCAAGACACACATTTTCCGCGCTGCTTGCACACAAGACTTCACCCGC 780 725 TTTAGTTTCTGCTTGCAGGCGAACACACACACACACACAC	
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FEATURES COMMENT

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PIPPADLGTREGSSVHPALEAQTGESQILPDVTTKTWGFNGTHLGFTLVVKKGDDVHV
DVINNILDEMTTVHWHGHWCLPALDAGGHRSPLGOGGVWSFTWVANDAATLWTHPHTHG
LTGLHAYRGLAGMITVBDEATDKLDLPREVGYDDIFLVLMWRFTWARDAETPROTEDLPDL
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EPQDRTTLAIGFGERNEITVWELEPEDVILDARSCYFEDWYGYDDEWFDYDFGNSDFQL
LTTGPSDDAAQAPALPGVVKSTEPDVILDARERFFINNTFSLNDLGMWQRVDVVID
LTTGPSDDAAQAPALPGVLVKSTEPDVILDATERFRFINNTFSLNDLGMWQRVDVVID
AVEFGHYPDDPGWBYNTHCHMLXHEDQGRWGQFVITVEBGFBRAVLGSGTGSSIDSAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /procein_id=BAB98337.1"

/db_xref="G1:2132371.1"

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rIGR00960:3a0501s02: Type II (General) Secretory Pathway
(IISP) Family protein
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                          Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida, Tokyo 194-8533, Japan (E-mail:snakagawa@xanagen.com, Tel:81-44-829-3031, Fax:81-44-813-1651)
This sequence is conducted by collaboration of Kyowa Hakko Kogyo Co. Ltd. And Kitasato University.
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'trans1 table=11
'product="Putative multicopper oxidases"
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/db_xref="G1:21323712"
                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="ATCC 13032"
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/gene="Cgl0944"
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/gene="Cg10945"
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                                                                                                 329478 TABABCATCTCCACGCGCAGCAAGGATAATGTGTGCGCTTCATCTTCCAAGCGCACGT
                                                                                                                                                                      329418 GAGCGTTGCTCCACCCCAAGAAGCTACCTCGTTGAACACACGGAGGAAACCATGTGGATAG
                                                                                                                                                                                                                                                                                                                              TTAGTTTCTGCTTGCAGCAGCAGCATTTTCCGCGCTGCTTGCAGAGACTTCACCCGC
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                                                                        TAAAACATCTCCACGCCGCAGCAAGGATAATGTGTGCGCTTCATCTTCCAAGCGCAGCGT
                                                                                                                                                 GAGCGTTGCTCCACCCCAAGAAGCTACCTCGTTGAACACGGGAAACCATGTGGATAG
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/transl table=11
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system, ATPase component"
/protein_id="BABB9345.1"
/protein_id="BABB9345.1"
/bxef=-01:2123719*
/translation=-WARTTHTASSILREWIRRORGKVAFGAFFLGWWGLSEALVPIAI
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GLIVULVPIISGYNALPREGNERSTADADSSTRIFGQIGTGVSAARGFGAATURISDWIX
GLIVULVPIISGYNALSKGISTRANGTGATASGGAATURICADATIVILISDWIY
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                                                                                                          LASDSTEILNLYRDEVNGYVPEDQSHVVNGYIDSIAGSAAAGQYGVAVGVITALMTSS
YVRASERCANAYVGRSGERTLIKRAALLIFULALLIGIIIILVGYRULNETYNGIF
APIAEPLHITNULSELTDRENPINIWKEPVIVGYLINGYLIKYRALDKERWERML
SLGSFLAIVGILLAGVGLNEYFILFAAFSSYGAVGSLLAVFIALMVFNICLIIGIKIN
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ORGANISM Corynebacterium glutamicum Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterinea; Corynebacteriume; Corynebacteriume; Corynebacteriume; AUTHORS Kim,J.W., Lee,H.S. and Hwang,B.J. TITLE Corynebacterium glutamicum genes encoding metabolic pathway Corynebacterium glutamicum genes encoding metabolic pathway TOUTHORS AUTHORGESELICSTAFT (DE) FEATURES 1. 993 Cost on Journal field and and and and and and and and and an	OY 542 AAAACATCTCCAGGCAGGAAGATATGTGTGTGTGTGTGTG
122 TCTGTGAGTCTAGGTAGAATCTAGATTCCAGGCGCCATCGTTGCCAATACATCGTTGT 181	RESULT 6 AX244055/c AX244055 LOCUS AX244055 DEFINITION Sequence 47 from Patent WO0166573. ACCESSION AX244055 VERSION AX244055 SOURCE COTYNEbacterium glutamicum

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              90 CGAGGGGGAAATGGAAAGGCTAAGGAGCGCCTTCGAAGCTGCCTTCATCATGATTGA
                                                                                                                                                                                                                     Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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/note="unnamed protein product; RXA01394"
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                                                                                                                                                                                                                                                                                                                                                                                       /organism="Corynebacterium glutamicum"
|mol_type="unassigned DNA"
|db_xref="taxon:1718"
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                                                                                                                                                         DNA
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BASF AKTIENGESELLSCHAFT (DE)
Location/Qualifiers
                                                        GAGCAAAGTGTCCAGTTGAATGGGGTTCAT 954
                                                                                                                                                     822 bp
Sequence 53 from Patent WO0100843.
AX063771
                                                                         30 GAGCAAAGTGTCCAGTTGAATGGGGTTCAT
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                              GOIN33/569,GOIN33/68,GOIN37/00//C12P21/08,(C12N1/21,C12R1:15),
(C12N1/21,C12R1:13),(C12N1/21,C12R1:01),(C12P13/08,C12R1:15),
C12N15/00,
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CL2P19/00,CL2P19/34,CL2P21/02,CL2Q1/37,CL2Q1/68,G01N33/53,
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Location/Qualifiers
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100.0%; Pred. No. 9.5e-203;
tive 0; Mismatches 0;
                                                                                                               Location/Qualifiers
                                                                                                                                                                        1. .870
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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                                                                                                      Novel polynucleotide
                                                                                      C12N5/00,C12N15/00
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     PC 04,C12P1
PC C12P13/0
G01N33/566,
PC G01N33/5
PC C12N15/0
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Corynebacterium efficiens YS-314 DNA, complete genome, section
                                                                                                                                                                      1045 TCTGCTTTTGGGGGCCAGTCTTTTACTGTCCATCGGACCGCAGAATGTACTGGTGATTAA 1104
                                                                                                                                                                                                                                                                                                            CTTTTTGTTCATCGCCGGCACCTTGGCGGTGATCTTTTGTCCAATGCCGCCCGATCGT 1224
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Corynebacterium efficiens YS-314
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
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                                                                                                                                                                                                                                                                                       1525 CGGCGCGCAATACGGCGACACGGAGGAGGTTTTTCGCCGCTGGCGCGTTCGCGGAAG 1584
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                                                                                                                                                                                                                                                                                                                                                                              1645 CCCCAAGGIGTGGCGCTGGATCAACGTCGTGGCAGTTGTGATGACCGCATTGGCCAT 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 780
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Corynebacterium glutamicum genes encoding metabolic pathway
                                                                                                                                                                                                                                                                                                            1585 CCTGATCTGGTTCCCGCTGGTGGGTTTCGGCGCAGCAGCATTGTCACGCCCGCTGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       721 CCCCAAGGTGTGGCGCTGGATCAACGTCGTGGCAGTTGTGATGACGCGCATTGGCCAT
                                         361 GAAAGACGCCATGACAACAAGATGGAAGCGCCACAGATCATTGAAGAAACAGAACCAAC
                                                                               1345 CGTGCCCCATGACACGCCTTTGGGCGGTTCGCCGCTGGCCACTGACACGCGCAACCGGGT
                                                                                                  GCGGGTGGAGGTGAGCGTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAAT
                                                                                                                                                                           481 GCGGGTGGAGGTGGAGCGTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAAT
                                                                                                                                                                                                                   1465 CGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCGTTTGTGTGTTTATCGGCGGCGT
                                                                                                                                                                                                                                                   541 GGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCGTTTGTGTGTTTATCGGCGGCGT
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.6%; Score 822; DB 6; Length 822; 100.0%; Pred. No. 6.1e-191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Corynebacterium glutamicum"
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| Adb_txref="taxon:1718"
| Adb_txref="taxon:1718"
| Adb_txref="taxon:1718"
| Adb_txref="taxon:1718"
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BASF AKTIENCESELLSCHART (DE)
Location/Qualifiers
1. .822
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Sequence 51 from Patent WO0166573.
AX244059
AX244059.1 GI:15859123
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Best Local Similarity
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COMMENT

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/translation="MRTTGVKKALLGIVAVLGSGLLVACGSVDPNRFEPHPRQVAEGK
ENLYTAVDPYLGINVISELKKTVLGNRGRFAVIRHEDNLIADPFDPLNEGTSDLVIG
CTGALLEVVNPVLAGELEEETLAAVEAGETDINSGEMRDRTFDALIGSLPSRLDTADP
SNAGGCPGANGLEVYPTVPIYRNPTFSRADREILNWASGALTTSELQELIEEAKELGRS
RELVKEFVASKGG"
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DNEFPVAELTIVGYDLMEVFITYTGRLIWGRVLAGGAASGAWLGLFFGLYMGLVSKLMF
SSLLIGLVMGVVFGVVLAAVPYWASRGKRDFTSATQIVAGRYDILGRPDRAREARDMI
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QELSEDRQAELI FILLIAGFEDWRAADVAKELYGLERDRGAVLLELMDERLADIL
QELSEDRQAELI FILLI FERADVLEEMDEDAADLIGELEBDKAGVLLELMDERSAP
PTGKAGRREDPWATPEPLYMD PSITVARALAMARNPOLPTSLASLVEVVREPTAT
PTGKYLGCVHLQXLLREPPSSLVGGILDPDLPPLYANDSGETAARFFATYNLVCGPVL
DENGHLIGAVAVDDLLDHMLPEDWRDAGIRPGVKEETLG"
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LGIVVELVNNKRRIFLPMIRIALBPKRVNLISGSVSLRSFKARTGELQVIGDLIGTK
VHTDDPELEQLHGRAVEIADVELEQTRIRDMVISRVALIGERPKFGRRPTLYIAPWSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="Wadysrsdidtelygtkrrrrrrdddtygayarkyarffgtggy
lfwgtifyliwimlanggfawnwdpypfiliniafstgaayaafillagnrgedrdk
stiladrrrabetkadtbfltrelagyrlaygemytrdylrhelddlrgflerleakl
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPMYTGSLENRLGGGGDAQPVRNEITRDDLLSLSLLDVPVPGLQVVQLLEPPEDAQSI
DLEEVVTRDYTAYELPYDLEQIRGILASIPTDVGLASKKAAEHLDAGNLWTALRRNG
PGPTRVSKLIARKRPKLFPIFDSAIKRQLMTNSVGFYENFHTVLRAEDKALSRHLKGI
                                                                                                      IGSDARENGVODMINEPOAHGVIMISIAHFYBGANARVVRRGPMIHRAIQOFLSDVFWG
DLDILLLDLPPGTGDIAITIAGLLPNRALLIVTTPOAAAADVABRAGSISLGTRQKVA
GVIENKSAMVRDDGSTRAFVEGGGGGEKIAQRLSMLTGEDVPULGSVPLDPSLRVGGDV
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COMPLEMENT (2513. .3271)
                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
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db_xref="G1:23493020"
/translation="MMSQVTESAVRSALSRVEDPEIGKPITELGMVKSVAIDGSDVQV
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/note="CE1184, similar to AE007003-4|AAK45528.1| percent
identity: 52 in 417 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTERADOSGNSALADISTIRVEDVVVWMADHKRT"
complement (3282. .3836)
/note="CE1183, similar to AE007003-3|AAK45527.1| percent
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|protein_id="BAC17995.1"
|db_xref="GI:23493024"
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/transl_table=11
/produci="conserved hypothetical protein"
/protein_id="BAC17933.1"
/db_xref="G1:23493022"
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/rransT table=11
/product="conserved hypothetical protein"
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/db_xref="GI:23493023"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identity: 57 in 159 aa"
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/transl_table=11
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note="CE1186"
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NNAKQNLDTDFGEEFPDEIRKPMAQIAQIRSMSPKTAITRALFDGDDSFLDSFDPKKIM
ADDTAGQAHRQQVAKTGTTPEHAEVVERPADRIDFTQSPNTFGKNNDGGKPPAGGGYT
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identity: 63 in 370 aa"
                                                                                 Comparative Complete Genome Sequence Analysis of the Amino Acid
Replacements Responsible for the Thermostability of Corynebacterium
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'note="CE1180, similar to AJ292256-1|CAC21724.1| percent
identity: 26 in 155 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hachioji, Tokyo, 192-0392 Japan
Nishio, Y., Usuda, Y. and Sugimeto, S. are at the Ajinomoto Co.,
Inc., Kawasaki, Kanagawa, 210-8681 Japan
Tre other authors are at the National Institute of Technology and
Evaluation, Shibuya-ku, Tokyo, 151-0066 Japan.
                                                                                                                                                                                                                                                                                                                                                               Submitted (17-MAY-2002) Director-General of Biotechnology Center, Submitted (17-MAY-2002) and Evaluation, Biotechnology National Institute of Technology and Evaluation, Biotechnology Center; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Tapan (E-mail: BioGmitte.go.jp., Pel.81-3-3481-1933, Fax:81-3-3481-8424) Kawarabayasi, Y is officially affiliated with the National Institute of Advanced Industrial Science and Technology, Tsukuba, Ibaraki, 305-8566 Japan
                  Sugimoto,S., Matsui,K., Yamagishi,A., Kikuchi,H., Ikeo,K. and Gojobori,T.
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/protein_id="BAC17991.1"
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Director-General of Biotechnology Center.
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(protein id="BAC17988.1"
db_xref="GI:23493017"
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22723752
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/strain="YS-314"
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/note="CE1178"
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/transl_table=11
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/transl_table=11
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/note="CE1179"
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                                     TITCCCATCAACCATGTAGGCATCCCGCAATGAGGGGGTTGCAATGGCCAAGTGGCGCAT
                                                                                                                                                                              541 TAAAACATCTCCACGCGGAGCAAGGATAATGTGTGCGCTTCATCTTCCAAGCGCAGCGT
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                                                                                                                                                                                                                                                                                                                     /kb_xref="GI:23493027"
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GGGGTHNGNNDEVTQSDQAIAAGNLALSAADGKWTINGQDVVDNNVNAVKVVPGDTLV
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SGNTYTFEGQVRGSGVSALSIKQAA"
complement (8190. .9443)
/nore="CEN189", similar to AF024666-23 | AAG03374.1 | percent
identity: 84 in 408 aa"
                                                                                                                       /translation="METILIGVILPVAACVQGAIGFGLGMLAAPITALMRPDLLPGDLI
LLAFGFSLATWARDREWFWYNDVGWSLLFGFTPRSVLGFWAVAMVRACHKTVATAV
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VCFVIGSAISIALLTGAGALGMMHLQAALVYAPAVIAGYFLSGVVNKHLNRRLIFIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="transposase"
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/bx xref="4f1:23428"
/translation="MAAGPYSIDPTTYLDELLAQASPDLMREMLQGFINQILSTQADQ
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DLARAGIARVILVTSDAHLAIGHALDARAMOMORTHISKRILYRYSKTYVAVSKTOMPTLA
AMETIT EQQDANGSVWGAREVVAFCEGRFPDYADYLEBALDELAFTNAPKSVWTKV
WSNNPTERLINREIRRRTDVVGI FPNRDAVVRLVGAVLAEQHDDWIQQKRYMSLISLEQ
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ALTTVIATCYLKGVSTRRMNDLVATLGINNLSKSQVSDMAKDLDQMVEEFRTRPLDTG
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 note="CE1187, similar to AE007262-3[AAK65408.1| percent
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                                                                      'producE="conserved hypothetical protein"
protein id="BAC17997.1"
db xref="GI:23493026"
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Pred. No. 7.8e-190;
0; Mismatches 524;
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trans[ table=1
product="hypothetical protein"
protein id=PBAC17998.1"
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complement(11439. .15143)
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note="CE1188"
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Whitehead, S. and Barrell B.G. Parkhill, J. The complete genome sequence and analysis of Corynebacterium diphtheriae NCTC13129 Nucleic Acids Res. 31 (22), 6516-6523 (2003) 2 (bases 1 to 349535) 2 (bases 1 to 349535) Direct Submission Direct Submission Cordeno-Tarraga, A.M. Direct Submission Cordeno-Tarraga A.M., submitted on behalf Submitted (03-0CT-2003) Cerdeno-Tarraga A.M., submitted on behalf of the Pathogen Sequencing Unit, Sanger Institute, Wellcome Trust Genome Campus Hirxton, Cambridge CB10 18A E-mail:	/db_xref="harcorcili2" /db_xref="taxon:171" /note="hiotype gravis" 76402 /locus_tag="DIP1058" 76402 /locus_tag="DIP1058" /note="similar to Mycobacterium tuberculosis hypothetical 11.0 kba protein Rv1898 or MT1949 or MTCY180.20c SW:Y198_MYCTU (007734) (102 aa) fasta scores: B(): 5.8e-16, 56.43 in in 102 aa, and to Aquifex aeolicus hypothetical 17.9 kba protein AQ. 2067 TR:067847 (EMBL:AE000771) (157 aa) fasta scores: B(): 4.7e-08,		(58 02%)" complement (4051226) /locus tag="DIPL059" complement (4051226) /locus tag="DIPL059" /locus tag="DIPL059" /nocus tag="DIPL05" /nocus tag	~~~~
Whi TITLE The dip JOURNAL Nuc PUBMED 146 REFERENCE 2 AUTHORS CEX TITLE DIX JOURNAL SUB JOURNAL SUB GEN FEATURES	gene CDS	misc_feature misc_feature	gene CDS	misc_feature misc_feature
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GTGTCCAGGTGGGTTCATGAAGCAATTCTAAACCATGTTCAGTCTCTATCATTTT ACTTAAGTACTTCCATAGGTGATCATGAAATCTTCATTCA	TICACCCTCGGCACCCTCGGGGTCGGCCTGATCTCCGACCGCCCCGATCATTCTCGAC ATTATGCGCTGGGGTGGCATCGCTTACGTTTGCCGTCATGGCAGCGAAGGA ATTATGCGCTGGGGGGGACGCTACCTGCTTATGGTTTGCCGTCATGGCGGCGCGGAGG ATCCTGCGCTGGTGGGGGACGCCTACCTGCTGTGGTGTGGGGGTGATGGCGGGCG	1412 GAGGTGAGGGGGGGGTTGGGGTAAGGCCANGTGGGGAGGGGGTGGTGGTGGGGGTGGGGGGGGGG	42 TGGTTGCCACTGGTCGGTTACGGCGCGCCCCTGTCGCGTCCCCTGTC 52 GTGTGGCGCTGGATCAACGTCGTCGTCGTGTCGTTGGCGTGCGCGCGC	HX24815/T S49515 bp DNA linear BCT 06-NOV-2003 segment 4/8. N. Corynabacterium diphtheriae gravis NCTC13129, complete genome; segment 4/8. BX248357.1 GI:88199912 Complete genome: Corynabacterium diphtheriae Corynabacterium diphtheriae Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynabacterium diphtheriae Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynabacterium diphtheriae Bacteria; Actinobacteria; Actinobacteridae; Corynabacterium diphtheriae Corynabacterium diphtheriae Bacteria; Actinobacteriae; Actinobacteridae; Corynabacterium diphtheriae Corynabacterium diphtheriae
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37897 GAİCCAACAGCTTCGGACTİĞCCACTĞCAAAATATCĞGAATĞCACCTAACGCTATCGAGT 37838
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                                                                                                                                                                                                                                                                                                                           /locus_tag="DIPI061"
/nocus_tag="peptide predicted for DIPI061 by SignalP 2.0
/noce="Signal peptide probability 1.000) with cleavage site
probability 0.663 between residues 34 and 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 IGGGACCGAAGCGTAAGACGGGCATCGCAGCCCAATCTAGTTTCCCATCAACCATGTAGG 440
                                                                                                /tranglation="Mirqpryrlplpivitriviillctiimslgvgarnitspdila
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                                                                                                                                                                                SALLTGIGDGISLVNPQAFDRLKSWMVGNIDAGSYQPAAVAGYGLILGILVTATCMRQ
LNALSLGDELAITMGASIAKTRLFTFIAIVVLAASATAAAGVITFLGIMVPHIARMIV
                                                                                                                                                                                                                                GPNILRLVATASLIGPIIVLSADILGRIIVPGEFPAGVVVAFIGAPFLIAYAQTKRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jocus tag="DIDI062"
/locte="Similar to Escherichia coli iron(III)
dicitrate-binding periplasmic protein precursor FecB or
B4290 SW:FECB_ECOLI (P15028) (300 aa) fasta scores: E():
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441 CAICCCGCAATGAGGGGGTTGCAATGGCCCAAGTGGCGCATGGTTCCAAGTTCTACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 GCCTGCGCCCCACAGACCATCGACGCCCGTCCAGGTCTTGAAGCACATCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 GGAGGATCACTICICCTGCTTTTAGCATGGGAGCAGCTTGGGGTTTCGGGAAGAAGTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 AACCAAGGCTCGGCGAATTGCCTCACCAAAACCTTCCGCCGACGGGACAATGGATACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                 signal-peptide site"

signal-peptide site"

complement(2199. .255)

/locus aga="mlpl061"

/note="BlastProbom hit to PD001557, PD001557"

/note="mlastProbom hit to PD001557, PD001557"

/locus raga="mlpl061"

/note="HPMPfam hit to PF01032, PecCD transport family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              order (complement (13096. 3161), complement (2334. 2990), complement (2838. 2903), complement (2766. 2831), complement (2870. 2755), complement (2544. 2609), complement (3344. 2459), complement (2213. 2459), complement (211. 2216),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 AICTAGAITICCAGGGGGCATCGTIGCCAAIACAICGGTGTGTGAATGGGTATCTCAICGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="9 probable transmembrane helices predicted for DIP1061 by TMHMM2.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
product="Putative iron-siderophore uptake system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 349535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.5%; Score 724.4; DB 1;
58.2%; Pred. No. 1.2e-166;
tive 0; Mismatches 931;
                                                   /protein_id="CAE49584.1"
/db_xref="GI:38199916"
                                                                                                                                                                                                                                                                                                 complement (3090. .3191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus tag="DIP1061"
/note="9 probable tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus tag="DIP1062"
3239. .4282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 1351; Conservative
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OMRIPRVYGILVGAALALAGSLEGSLTRNPLGSPDIGFSTGATTVVM
OMRIPRVYGILVGAALALAGSLEGSLTRNPLGSPDIGFSTGATTGVILAFELLD
FALSAAGNGLRWHIATEACCTLAILITTTIPLRFLDVLSLGDDLAVGLGLR
LQLTKLLLLVGGYFLVAATTAAGPTAFVALASFHIARALITSSARTPLVETSVIGALL
ITVAALGGGRLFYPTOLVGVGYFLWATTATGGRYLLMLLARGSKENS"
complement (2108. .2182)
/locus tag=DIPP1060.
/note="Signal peptide predicted for DIP1060 by SignalP 2.0
HWM (Signal peptide predicted for DIP1060 by SignalP 2.0
HWM (Signal peptide probability 0.966) with cleavage site
probability 0.180 between residues 25 and 26;
signal-peptide site"
complement (1244. .2116)
/locus tag="DIP1060"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E(): 8e-36, 36.53% id in 323 aa, and to Becherichia coli
ferric enterobactin transport system permease protein fepD
B(): 5.2e-40, 40-37% id in 322 aa"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iron-siderophore uptake Bystem transmembrane component
sci51.27C TR:Q9S213 (EMBL:AL109848) (348 aa) fasta scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iron-siderophore uptake system transmembrane component sci51.26C TR:09S214 (EMBL:ALI09848) (375 aa) fasta scores: E(): 5e-40, 40.74% id in 324 aa. and to Escherichia coli ferritc enterobactin transport system permease protein fepg fepg or B0589 SW:REPG ECOLI (P28877) (330 aa) fasta scores: E(): 1.8e-45, 44.09% id in 322 aa.
                                                                                                                                                                                                      'note="ScanRegExp hit to PS00211, ABC transporters family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //orce="HAMPfam hit to PF01032, FecCD transport family" order[ormplement(2105. .2161), complement(1979. .2044), complement(1883. .1939), complement(1805. .1870), complement(11803. .1939), complement(1607. .1657), complement(1445. .1510), complement(1445. .1530), complement(1247. .1303))
                                                                                                                                                                                                                                                                                                                                                       complement(1086. 1109)
/locus tage="D1P1059"
/note="ScanRegExp hit to PS00017, ATP/GTP-binding site motif A (P-loop)."
complement(1223. .2182)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compare tage "DIP1060" /note="9 probable transmembrane helices predicted for DIP1060 by TWHWM2.0"
                                                complement (579. .797)
/locus tag="DIPL056"
/note="ProfileScan hit to PS50100, 2nd half motif for nucleotide binding associated with P-loop."
/complement (753. .797)
/locus tag="DIPL059"
                                                                                                                                                                                                                                                    complement(1047. .1124)
/locus_tag="DIP1059"
/note="ProfileScan hit to PS50101, P-loop nucleotide
binding motif (does not find all)."
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/note="Similar to Streptomyces coelicolor putative
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/note="Similar to Streptomyces coelicolor putative
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                   'note="HMMPfam hit to PF00005, ABC transporter"
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/locus tag="DIP1060"
/note="BlastProDom hit to PD001557, PD001557"
complement (2184. .3191)
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/protein_id="CAE49582.1"
/db_xref="GI:38199915"
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complement(2184, .3191)
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complement(1223. .2182)
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                                                                                                                                                                                                                                              signature
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1616 GCAGCAGCATTGTCACGCCCGCTGTCCAAGCTGTGGCGCTGGATCAACGTCGTC 1675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTCTTCTCGGGGATTTCTGACGTCTTTTTGTTCATCGCCGGCACCTTGGGCGTT
                                                        Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K., Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
Novel polymucleotides
Patent: EP 1108790-A 3455 20-UJN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1676 GIGGCAGIIGIGAIGACCGCAIIGGCCAICAAACIGAIGIIGAIGGGI 1723
                                                                                                      Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 708
                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                    1. 708
forganism="Corynebacterium glutamicum"
/mol_type="unassigned DNA"
/db_xref="taxon:1718"
                                                                                                                                                                                                                                                                                                                         29.8%; Score 708; DB 6; Lk
llarity 100.0%; Pred. No. 6.5e-163;
Conservative 0; Mismatches 0;
Sequence 3455 from Patent EP1108790.
                                  GI:14041027
                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 708; Conserv
                                   AX123539.1
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                     ACCESSION
VERSION
KEYWORDS
SOURCE
        DEFINITION
                                                                                                                                              AUTHORS
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                                                                                                                                REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1616 GCAGCAGCATTGTCACGCCCGCTGTCCAAGGTGTGGCGCTGGATCAACGTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 11-MAY-2001
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                                                                                                                                                          /trānslation="MVIMEIFITGELLEGASLILSIGPQNVLVIKQGIKREGLIAVLLV
CLISDVFLFIRGTLGVDLSNAAPIVLDIMRMGGIAYLLMFANMAAKDAMTNKTEAPQ
IIEETEPTVPDDTPLGGSAVATDTRARYKTGYSVDKQRVWVKPMLMAIVLFMLNPNAY
UDAPYFIGGVGAYGYGDTGRMIFAAGAFAASLIMFPLVGFGAAALSRPLSSPKVWRWIN
VVVAVVMTALAIKLMLMG"
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/db_xref="G1:28550159"
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                               GenCore version 5.1.6
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ACA26879 ACA38559 AAT33536

This DNA, isolated from Corynebacterium glutamicum, contains the LysG, plysB and ORR3 genes. LysG and LysB encode a lyseine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity amino acids (A) is improved by increasing the export-carrier activity. The method is specifically used to increase production of lysine, used as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Sequence has been found to depend on a single gene. NB. This sequence has been created from the information given in table 2 of the specification

Sequence 2374 BP; 526 A; 640 C; 648 G; 560 T; 0 U; 0 Other;

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S ed	841 AGCTTTAACGCGCTGACTCACCGCCGAGGGGGAAATGGAAAGGGCTAAGGAGGCCTTC 900
ð	AGCT 9
ΩÞ	GAAGCTGCCTTCATCATCATGATTGAGACAAAGTGTCCAGTTGAATGGGGTTCATGAAGCT 9
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හි සි	1141 TCTCGTGTGTTTAATTTCTGACGTCTTTTTTCATCATCGCCGGCACCTCGGGCATTGATCT 1200 1141 TCTCGTGTGTTTAATTTCTGACGTCTTTTTGTTCATCGCCGCACCTTGGGCGTTGATCT 1200
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qq	21 GATCATTGAAGAAAAAGAACCAACGTGCCCGATGACACGCCTTTGGGCGGTTCGGCGGT 138
ò	81 GGCCACTGACACGGCCAACCGGGTGCGGGTGGGGGTGAGCGTCGATAAGCAGCGGGTTTG
q ₀	
Š	1441 GGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGA 1500
qq	41 GGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGA 150
ð 1	1 CGCGTTTGTGTTTATCGGCGCGTCGGCGCGATACGGCGACACCGGACGGTGGATTTT
<u>a</u>	01 CGCGTTTGTGTTTATCGGCGGCGTCGGCGCGCAATACGGCGACACCGGGGGATTTT 156
දු ද	1561 CGCCGCTGGCGGCGCGCGCAAGCCTGATCTGGTTCCCGCTGGGTTTCCGCTGGCTTTCCGCTGGCTTTCCGCTGGCTTTCCGCTGGCTTTCCGCTGGCGCAGC
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7 සි	21 AGCALTGARGCCCGCTGCCCAAGSTGTGGCGCTGGATCAAGSTGTGGC
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                  The present invention relates to a method for producing L-arginine in a microorganism (e.g. coryneform bacteria) that has L-arginine producing ability and has been modified for enhanced expression of the 1y8E gene. The microorganism is also modified so that an arginine repressor (argR) does not function normally. The method of the invention is useful for the promoting agents, amino acid infusion and comprehensive amino acid pharmaceuticals. The present sequence represents a DNA fragment containing Corynebacterium giutamicum LysG and LysE genes. Note: The present sequence is given as SEQ ID No:24 in the Sequence Listing but is referred to as SEQ ID No:25 in the rest of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 GGITCCAAGIICIACIACIACITCACATCCCGCCACGGGATTAGCIICACGGGITACCTCC
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                                                                                                                                                                                                                   Query Match 100.0%; Score 2374; Best Local Similarity 100.0%; Pred. No. 0; Matches 2374; Conservative 0; Mismatches
     Example 4; Page 26-27; 36pp; English
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                                                L-arginine production; coryneform bacteria; lysE; arginine argk; liver function promoting agent; amino acid infusion; amino acid pharmaceutical; LysG; ds.
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me, account invention provides a number of nucleotide and protein	The present inventors from the Coryneforms sequences from the Coryneform bacterium Corynebacterium glutamic sequences from the Coryneform the mutation point of a gene derived		Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino	acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described				red. No. 0; Mismatches 0:	Matches 23/4; Combelvative v; http://docco.co	7	129968	129908	121	129848	181 GTCAATGGGTATCTCATCGAGGAGGATCACTTCTCCTGCTTTTAGCATGGGAGCAGCTTG	129788 GTCAATGGGTATCTCATCGAGGAGGATCTCTCCTGCTTTTAGCATGGGAGCAGCTTG	241 GGTTTCGGGAAGAGTCCCCAACCAAGGCCTCGGCGAATTGCCTCACCAAAACCTTCCGC	129728 GGTTTCGGGAAGAAGTCCCCAACCAAGGCTCGGCGAATTGCCTCACCAAAACCTTCGG		129668 CGACGGGACAATGGATACGCGCCTTGCGCCCCCCAAAGAACAATCGAACGCGCCCCCCCC	361 ACGCTCTTGAAGCACATCTTTGGGACCTAAGACGGCATTGGAGCCATACAACAACAACAACAACAACAACAACAACAACAACA		421 TITCCCATCAACCATGTAGGATCCGGCATGAAGAGGGATGGAGGGGTGGAAGAGGGATGGGCATGGAAGAGGGATGGGCGATGGAGGGATTGGAATGGCCAAGTGGCGCAT	DD 1239%9 IIICCAAAAFTCTACTACTTCACATCCCGCCACGGGATTAGCTTCACGGGTTACCGCTCC 540	129488					Qy 661 CGAATCTGCGTTGATGACGATGATTAACGGGATTTCAGCAAGGCGTCCAGATAGTTGCCC 720	CGAATCTGCGTTGATGGCGATGGTTAACGGGATTTCAGCAAGGGCGTCCAAAAAAAA		DD 129488 IIIAGIIIGGCCGGTIGGGTGCGGATACCAACACTCGACCCACGTGATGCTCGAG 840 Qy 781 TTCGGTTGGTTTGGCCGGTTGGGTGCGGATACCAACACTCGACCACGTGATGCTCGAG 840
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GOGGTTCGCGGCAAGCCTGATCTGGTTCCGCTGGTGGGTTTCGGCGCAGC 1620 PAGGCCGGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGC 1680 CATGITGATGGCAATGGGGGGACCTGGTTGAACCGGAATGCGTATTGGA 1500 128589 acgaaggaccaatcaatgcactggtcacggtatccgcgccgtactctccttg 1920 129069 GACCGCATTGGCCATCAAACTGATGTTGATGGGTTAGTTTTCGCGGGTTTT 1740 129009 128949 1440 GITTATICGGCGGCGGCGCAATACGGCGACGGCGGGCGGTGGATTTT 1560 1380 GCGGGGCGATGGTGCTCGATATTATGGCTGGGGGGGCTGCCTTACCT 1260 1080 1140 1200 1020 900 ACGCGCAACCGGGTGGGGGGGGGGGGGCGTCGATAAGCAGCGGGTTTG AGAAACAAACCGTGCCCGATGACACGCCTTTGGGCGGTTCGGCCGTT ATCTTCATTACAGGTCTGCTTTTGGGGGCCAGCCTTTTACTGTCCATCGG TTAATTTCTGACGTCTTTTTGTTCATCGCCGGCACCTTGGGCGTTGATCT GTACTGGTGATTAAACAAGGAATTAAGCGCGAAAGGACTCATTGCGGTTCT CATCAATGATTGAGAGCAAAGTGTCCAGTTGAATGGGGGTTCATGAAGCT atgitaagaaccaatcatttacttaagtacttccataggtcacgatggt

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Best Local Similarity
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127868 GCCCTGCGCAAGTGGTGAGAAAGAATGACGCCAAGACCATTGTTGGCAGCTGACTGCAA 127809
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                                                                                     CTIACCCIGGCIGGCGCGGGAACCCTCTGGAATTCCAICGAGAIATTTGTCCGTGAGCAG 2100
                  CTCGCGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGGGTTCCTGGGGGGAT 1980
                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum MP protein nucleotide sequence SEQ ID NO:49.
                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
                                                                                                                                                        CAAGTICTCACCGTCATCGCCCGGTTCCTCCACCCAACGATTAATGATGGAATAGCTTGG
                                                                                                                                                                                          CTGATGAATCAGAAGCGGGGAGCCCTCCTCCGCCATGAACTCAGCCGCCTCCGCTGTGAG
                                                   1981 GICATIGAGCITGCGGACCATATCAATATTGTTCACGTTCAACATGCCCTCAGACAGGGA
                                                                                               carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds
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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microcraniams, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes
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100.0%; Pred. No. 4.9e-299;
tive 0; Mismatches 0;
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glutamicum gene #21 encoding metabolic pathway protein.
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                                                                                                             GITICGGGAAGAAGICCCCCAACCAAGGCCICGGCGAAITGCCTCACCAAAACCIICCGGC
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              TCAATGGGTATCTCATCGAGGATCACTTCTCCTGCTTTTAGCATGGGAGCTTGG
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The present invention relates to the isolation of movel Corynebacterium glutamicum genes encoding metabolic pathway (MP) proteins (AA711853-A471922). The metabolic pathway proteins of the invention include enzymes involved in the lysine and methionine biosynthetic pathways. The polymucleotide sequences of the invention can be used for the large-scale production and/or modulation of expression of fine chemicals such as lysine and methionine. The sequences of the invention may be used to identify C. glutamicum and related organisms e.g. C. diphtheriae in a identify C. glutamicum and related organisms e.g. C. diphtheriae in a subject to detect diphtheria. AAS96073.AAS96132 represent C. glutamicum genes encoding the novel metabolic pathway proteins of the invention
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Metabolic pathway protein; MP; lysine biosynthesis pathway; methionine biosynthesis pathway; large-scale production of Corynebacterium diphtheriae; diphtheria; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                 Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 207-208; 316pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      Schroeder H,
                                                                                                                                                                                                                                                                                      09-MAR-2000; 2000US-0187970P.
23-JUN-2000; 2000US-00606740.
                                                                                                                                                                                                                                          22-DEC-2000; 2000WO-IB002035.
                                                                                                       Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                         M, Kroeger B,
Lee H, Hwang B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding glutamicum, useful for
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Matches 993; Conserv
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Kim J, Lee
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AAS96096 standard; DNA; 993

AAS96096/c ID AAS960 XX

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TCCCGCCACGGGATTAGCTTCACGGGTTACCGCTCCTAAAACATCTCCACGCCGCAGCAA
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          Nakagawa S,
Tateishi N,
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                                                                                                                                              TTAGTITCTGCTTGCAGCAACACCATTTTCCGCGCTGCTTGCACAAGGACTTCACCGGCT
                                                                     AAAACATCTCCACGCCGCAGCAATAATGTGTGTGCGCTTCATCTTCCAAGCGCAGCGTG
                                                                              602 AGCGTTGCTCCACCCCAAGAAGCTACCTCGTTGAACACGGGAGGAAACCATGTGGAATAGC
                                                                                                         GAATCTGCGTTGATGGCGATGGTTAACGGGATTTCAGCAAGGCGGTCCAGATAGTTGCGCT
                                                     TTCCCATCAACCATGTAGGCATCCCGCAATGAGGGGTTGCAATGGCCCAAGTGGCGCATG
                                             GITCCAAGITCTACTACTTCACATCCCGCCACGGGATTAGCTTCACGGGTTACCGCCT
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                                                                                                                                                                                                                                                                            C glutamicum coding sequence fragment
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2000JP-00159162.
2000JP-00280988.
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325 GCGCCCAACAACCAACGACGCCCGGCCCAGGTCACGGTCTTGAAGCACATCTTTGGG 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 agariccagocorrogridocanacarogorogorangograroronacados 204
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100.0%; Pred. No. 1.3e-260;
tive 0; Mismatches 0; Indels
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                                             X,
                                                    Ochiai
                                                Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
(KYOW ) KYOWA HAKKO KOGYO KK.
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                                                                   90 CGAGGGGGAATGGAAAGGCTAAGGAGGCCCTTCGAAGCTGCCTTCATCAATGATTGA 31
                                                                                                                                                                                                                          Corynebacterium glutamicum, metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
                                                                                                                                                                                                            Corynebacterium glutamicum MP protein nucleotide sequence SEQ ID NO:53.
TAACGGGGATTTCAGCAAGGCGTCCAGATAGTTGCGCTTTAGTTTCTGCTTGCAGCAACAC
         CATITICCGCCCTGCTTGCACAAGGACTTCACCCGCTTCGGTTGCTTTGGCTTGGGTTGGGT
                                                        GCGCGATACCAACACTCGACCCACGTGATGCTCGAGAGCTTTAACGCGCTGACTCACGGC
                                                                                                                    GAGCAAAGTGTCCAGTTGAATGGGGTTCAT 954
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99DE-01031424.
99DE-01031434.
99DE-01031443.
99DE-01031443.
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99DE-01031541.
99DE-01031573.
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99US-0142101P.
99DE-01031415.
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99DE-01032186.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP mucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, mucleotides, lipids, saturated purine and atty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes
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Best Local Similarity 100.0%; Pred. No. 1.2e-245;
Matches 822; Conservative 0; Mismatches 0; Indels
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99DE-01033004.
99DE-01033005.
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99DE-01042087.
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03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of novel Corynebacterium gutamicum genes encoding metabolic pathway (MP) proteins (AAU71863-AAU71922). The metabolic pathway proteins of the invention include enzymes involved in the lysine and methicoine biosynthetic pathways. The polyynucleotide sequences of the invention can be used for the large-scale production and/or medulation of expression of fine chemicals such as production and/or medulation of expression of fine chemicals such as identify C. glutamicum and related organisms e.g. C. diphtheriae in a identify C. glutamicum and related organisms e.g. C. diphtheriae in a subject to detect diphtheria. AAS96073.AAS96132 represent C. glutamicum genes encoding the novel metabolic pathway proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                 985 TCATTTTACTTAAGTACTTCCATAGGTCACGATGGTGATCATGGAAAATCTTCATTACAGG 1044
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                            metabolic pathway proteins from Corynebacterium producing methionine and lysine in Corynebacterim
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                                                                                                                                                                                                                                                                 Sequence 822 BP; 167 A; 192 C; 246 G; 217 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                            34.6%; Score 822; DB 4; L4 ilarity 100.0%; Pred. No. 1.2e-245; Conservative 0; Mismatches 0;
                                                                                        Disclosure; Page 214-215; 316pp; English.
                                         acids encoding
WPI; 2001-582269/65.
P-PSDB; AAU71888.
                                                                                                                                                                                                                                                                                                               Local Similarity
                                                       glutamicum, useful
and Brevibacterium
                                                                                                                                                                                                                                                                                                                               822;
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                                                                                                                                                                 ACAAGGAATTAAGGGGGAAGGACTCATTGCGGTTCTCGTGTGTTTAATTTCTGACGT
                                                            GCTCGATATTATGCGCTGGGGATCGCTTACCTGTTATGGTTTGCCGTCATGGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metabolic pathway protein; MP; lygine biosynthesis pathway; methionine biosynthesis pathway; large-scale production of Corynebacterium diphtheriae; diphtheria; ds.
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2000US-00606740.
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H, Hwang B;
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Kim J, Lee E
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23-JUN-2000;
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181 GAICTTTTGTCCAATGCCGGCGGATCGTCGTCGATATTATGCGCTGGGGTGGCATCGCT
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Senoh A, Ikeda M, Ozaki A;
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07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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Tateishi N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to DNA encoding variants of protein with loop region and six hydrophobic helixes which facilitates excretion of L-1ysine and/or L-arginine to outside of cell of a methanol assimilating bacterium when introduced into the bacterium. The method is used for encoding a protein which facilitates excretion of L-lyaine, L-arginine or both of these L-amino acids to outside of a cell of a methanol assimilating bacterium when DNA of the method is introduced into the bacterium. The present sequence represents a lysE protein from Brevibacterium lactofermentum encoding sequence. (Updated on 27-OCT-2003
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                        1645 CCCCAAGGTGTGGGGGCGCTGGATCAACGTCGTGGCGGCTTGTGATGACGGCATTGGCCAT 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel DNA encoding variant of LysE protein from a coryneform bacterium, when introduced into methanol assimilating bacterium, facilitates excretion of L-lysine and/or L-arginine to outside of a cell.
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                                    cch 29.9%; Score 711; DB 8; Length 711; al Similarity 100.0%; Pred. No. 5.7e-211; 711; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 711 BP; 135 A; 173 C; 222 G; 181 T; 0 U; 0 Other;
                                                                        CAAACTGATGTTGATGGGTTAGTTTTCGCGGGTTTTGGAATC 1746
                                                                                    /*tag= a
/product= "lysE protein"
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1. .711
/*tag= a
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                                                                                                                                                                                                                                            LysE protein encoding sequence.
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                                                                                                                                                           ACC80941 standard; DNA; 711
                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum.
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(first entry)
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11-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a gene from a high temperature-resistant corporation microbe that encodes a heat-resistant lysin biosynthetic enzyme. The enzyme has aspartate-semialdehyde dehydrogenase activity and can be used for growing amino acid-producing microbes. The present sequence encodes an enzyme of the invention
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                                         1676 GIGGCAGITGIGATGACCGCAITGACCAAACTGAIGITGAIGGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heat-resistant; lysin biosynthesis; enzyme; coryneform; aspartate-semialdehyde dehydrogenase; lysE; ds.
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Best Local Similarity 68.4%; Pred. No. 7e-207;
Matches 1017; Conservative 0; Mismatches 454:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      temperature-registant coryneform microbe.
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                                                                                                                                                                                                                 RESULT 11
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                                                                                                                                                                                  Novel polymucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing
                                                                                                                                                                                                                        mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 708 BP; 134 A; 173 C; 221 G; 180 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 3455; 246pp + Sequence Listing; English.
                                                                                                              2001-376931/40.
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1136 GILCTICICGIGIGITIAATITCIGACGICTITITGITCAICGCCGGCACCITGGGCGIT 1195 1076 ATCGGACGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCG 1135 The present invention relates to DNA encoding variants of protein with loop region and six hydrophobic helixes which facilitates excretion of L-lysine and/or L-arginine to outside of cell of a methanol assimilating bacterium when introduced into the bacterium. The method is used for both of these L-amino acids to outside of a cell of a methanol assimilating bacterium when DNA of the method is introduced into the bacterium. The present sequence represents a lysE24 protein from bacterium and DNA of the method is introduced into the Brevibacterium lactorementum encoding sequence. (Updated on 27-OCT-2003 to standardise OS field) 61 ATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCG 120 Novel DNA encoding variant of LysE protein from a coryneform bacterium, when introduced into methanol assimilating bacterium, facilitates excretion of L-lysine and/or L-arginine to outside of a cell. 1016 AIGGIGAICAIGGAAAICIICAIIACAGGICIGCITITIGGGGGCCAGICIIIIACIGICC Length 712; 1472 Sequence 712 BP; 133 A; 173 C; 224 G; 182 T; 0 U; 0 Other; Indels 1426 GCCGTGGTGCTCACCGGATTGGCCGTGAAGCTGATCCTGATGGGTTA Score 696.8; DB 8; Pred. No. 1.6e-206; 0; Mismatches 2;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2146 GGCAGCTGACTGCAACAAGTTCTCACCGTCATCGCCCGGTTCCTCCACCCAACGATTAAT 2205
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  mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 627 GITTITGGGGGTITITIGGAATGGGGGCTITGGCCCCAAATGTIGAIGCCGGCGTGGGA
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03-AUG-2000; 2000JP-00280988.
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2291 TAGGAAGAAATACCCACGTAAAGAGCCTTTCCAGACGCAACAATGTCAACGCAATGCGTAC 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum). The typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation. AAR68082 and AAR68082 represent sequencing primers which are used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2231 AGAAGGGGGGAGCCTCCTCCGCCATGAACTCAGCCGCCTCCGCTGTGAGCTCTGGACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                 993 AGCACCAATCAATGCACTGGTCACGGTAATCCGGCGCGCGTACTCTCTTTGCTCGCGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCATGCAAGGGCCATCTGCGCAAGTGACTGCCCGCGTTCCTGGGCGATGTCATTGAGC
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drug design; gene.
                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                Length 993;
                                                                                                                                                                                                                       Sequence 993 BP; 222 A; 247 C; 277 G; 247 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                             Score 485.2; DB 4;
Pred. No. 2.7e-140;
0; Mismatches 3;
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20.4%;
Best Local Similarity 99.0%;
Matches 499; Conservative
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Best Local Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacteium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for
                                                                                                                                                                                                                       membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation; genome mapping; genetic engineering; ds.
                                                                                                                                                 Corynebacterium glutamicum MCT protein encoding DNA SBQ ID NO:669
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                                                                                                                                                                                                    Corynebacterium glutamicum; brevibacterium lactofermentum; MCT;
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99DE-01040832.
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99DE-01041378.
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99DE-01031478.
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P-PSDB; AAB76844

transformation

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(BADI) BASF

03-SEP-1999; 03-SEP-1999; 03-SEP-1999;

-AUG-1999;

4-JUL-1999

7-AUG-1999 -AUG-1999 27-AUG-1999; AUG-1999 31-AUG-1999; 31-AUG-1999, 31-AUG-1999; 03-SEP-1999;

27-AUG-1999

09-JUL-1999; 09-JUL-1999; 09-JUL-1999;

09-JUL-1999

09-JUL-1999

199-JUL-1999

2230

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2170

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06-SEP-2001; 2001US-00948993. 25-0CT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. (ELIT-) ELITRA PHARM INC. 'nά Wang |

The invention relates to an isolated mucleic acid comprission of the 6213 antisense sequencies given in the specification where expression to the 6213 antisense sequencies given in the specification where expression of the nucleic acid inhibits promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or its fragment whose expression is inhibited by the polypeptide; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding cantisense nucleic acid; (4) an antibody capable of specifically binding cantisense nucleic acid; (4) an antibody capable of specifically binding confiseration or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influence the activity of required for proliferation, or that inhibits cellular proliferation; (8) required for proliferation for callular proliferation of an equipment of a proliferation required gene product lies pathway in which the test compound that inhibits proliferation of an or a gene on which the test compound that inhibits are specifically or graduct is overexpressed or underexpressed; (12) determining the extent compound's activity; (11) a culture comprising strains in which the propertion or the ach of the strains is present in a culture or collection of compound; or (13) identifying the target of a compound that inhibits the 1730 TOGOGGGTTTTGGAATCGGTGGCCTTCGCCCAAATGTTGATGCCGGCGTCGTGGAAATC 1789 rėdranacericanaganarakaececedecenanininaritecnederecritedena 1035 proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryctic essential genee. Note: The sequence data for this patent did not form part of the printed specialication, but was obtained in electronic format directly from MIPO at fit, who. int/pub/published_pct_sequences New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. invention relates to an isolated nucleic acid comprising any one of Query Match
Best Local Similarity 67.1%; Pred. No. 3.5e-84;
Matches 433; Conservative 0; Mismatches 212; Indels 0; Sequence 1095 BP; 264 A; 247 C; 311 G; 273 T; 0 U; 0 Other; Claim 14; SEQ ID NO 17521; 1766pp; English. 2003-029926/02 P-PSDB; ABU25781 1094

TACTCTCCTTGCTCGCGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGCGT 1969

1910

1790 TCATCGATCGCCTCCAACTCGGCGTCAGAAACTCCAAGTTGTTGAGTGAATCAAGGCTG 1849

1034 grgicakiraraningcerrichangerrgakircangariraninakangrrecengarir 975

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Search completed: March 15, 2004, 14:59:10 Job time: 974.046 secs

2270 TCCGCTGTGAGCTCTGGACCGTAGGAAGAATACCCACGTAAAGAGCCTTTCCAGACGCA 2329 2210 GAATAGCTTGGCTGATGAATCAGAAGCGGGCAGCCCTCCCGCCATGAACTCAGCCGCC 2269 2149 2150 gergacigeaacaagricicacegrearegeessgricerecaaceaacaariaarg 2209 554 icrecediradricaderceanadeanadareceaeanaecanecerrecedarece 495 1970 ICCTGGGCGATGTCATTGAGCTTGCGGACCATATCAATATTGTTCACGTTCAACATGCCC 2029 734 rcadiraaaadcccccidigcaaddigdccaaaaardcaaraacacccadrccgrraricdcc 675 674 śchodcicznackagóriczicackarktricackagóriczriczakagóriczakara 615 854 cgraacdcraaarcarrcadrocacdcarcarcardaadarrrraagddrigaacarcrcr TCAGACAGGACTTACCCTGGCGGGGAACCCTCTGGAATTCCATCGAGATATTTG 794 traccchaddactrcccracracraccdrdaarccactdgacacgccccdaddatacctd 2090 recentraderadececracional de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia de la reconstancia della reconstancia de la reconstancia della reconstancia della reconstancia della reconstancia d 2330 ACAATGTCACGCAATGCGTACATGGTTTCTTCCAAAGGAGTATCT 2374 494 ACGAHGICTCGCAAAGCAHATGCAGTTTCTTCCAAAGGCGTATCT 450 2030 à g à g 8 ŏ q g ð g Š g

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

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RESULT 1
US-08-390-878-17/c
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Sequence 12, Appl.
Sequence 2, Applisequence 10, Appl.
Sequence 20, Appl.
Sequence 20, Appl.
Sequence 20, Appl.
Sequence 20, Appl.
Sequence 21, Appl.
Sequence 21, Appl.
Sequence 791, Appl.
Sequence 74135, Appl.
Sequence 744, Appl.
Sequence 744, Appl.
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22, Appl
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4674, Ap
1694, Ap
                                                                                                            March 15, 2004, 13:47:35; Search time 178.837 Seconds (without alignments) 7366.769 Million cell updates/sec
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1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*

7. /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*

7. /cgn2_6/ptodata/2/ina/packfiles1.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-920-812-20
US-08-920-817-20
US-08-920-827-20
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US-09-489-039A-4735
US-09-489-039A-4735
US-09-543-681A-791
US-09-553-991A-7644
US-09-252-991A-7644
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US-09-252-991A-7643
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US-09-252-991A-7643
US-09-252-991A-1393
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US-09-252-991A-14312
US-09-252-991A-14312
US-09-252-991A-14312
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US-09-103-840A-1
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US-09-894-844-12
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Listing first 45 summaries
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Sequence 1599, A
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Sequence 5423, App
Sequence 11957, A
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US-09-543-681A-800
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US-09-621-976-15639
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                                                                           APPLICANT: Stover, Charles K.
APPLICANT: Stover, Charles K.
APPLICANT: Stover, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,878
FILING DATE: 17-FEB-195
CLASSIFICATION WIMBER: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION WIMBER: 38 4.98
REGISTRATION WIMBER: 38 4.98
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543/5060
TELEPAX: 415/543/5063
TELEPAX: 415/543/5063
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15239 base pairs
TYPE: nucleic acid
STRANDENNESS: single
Sequence 17, Application US/08390878; Patent No. 5700683
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
COUNTRY: USA
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APPLICANT: Small, Peter
APPLICANT: Schoolnik, Gary
APPLICANT: Schoolnik, Gary
APPLICANT: Winderland Differences Between Species of
TITLE OF INVENTION: Molecular Differences Between Species of
TITLE OF INVENTION: the M. Tuberculosis Complex
FILE REFERENCE: STANIO2CON
CURRENT FILE STANIO2CON
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: 09/318,191
PRIOR PLING DATE: 1999-05-25
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; Sequence 12, Application US/09894844
; Patent No. 6686166
; GENERAL INFORMATION:
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Pred. No. 5.9e-26;
0; Mismatches 423;
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                                                                                 NIMBER OF SEQ ID NOS: 137
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
                                                                                                                                                                                                                                  TYPE: DNA
, ORGANISM: Mycobacteria tuberculosis
US-09-894-844-12
PRIOR APPLICATION NUMBER: 60/097,936
PRIOR FILING DATE: 1998-08-25
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Best Local Similarity 49.5%;
Matches 433; Conservative
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Pred. No. 9.8e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCATCAATGATTGAGAGCAAAGTGTCCAGTTG 942
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FLEISCHMAN, ROBERT D. APPLICANT: WHITE, Owen R. APPLICANT: FRASER, Claire M. APPLICANT: VENTER, John C. TITLE OF INVENTION: DNA SEQUENCES FORTILE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09103840A
Patent No. 6294328
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Best Local Similarity 49.5%;
Matches 433; Conservative
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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                                                                                                                                                                                                                                                 APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DIM SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
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Similarity 49.5%; Pred. No. 9.8e-24;
33; Conservative 0; Mismatches 423; Indels
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                         Sequence 2, Application US/09103840A Patent No. 6294328
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LENGTH: 4403765
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                                                                                                                              RESULT 3
US-09-103-840A-2
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                                                                                                                                                                                                                   Length 5541;
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Pred. No. 2.2e-19;
0; Mismatches 332;
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; Patent No. 5770375
                                                                                                                                                    ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-625
                                                                                                                                                                                                                             4.2%;
                                                                                               TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                           5541 base pairs
                                                                                                                                                                                                                                           Best Local Similarity 50.5
Matches 386; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                       TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                      SOURCE:
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US-08-920-827-20
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                                           LENGTH:
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                                                                                                                                        ORIGINAL
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                                                                             2229429 GCACCCGGCACCCGGCACCGGCTTCCGCTCGGTGGTCACCGCCGCCCATCGCCACCCTCT 2229488
           CTTTGGCCGGTTGGGTGCGCGATACCAACACTCGACCACGTGATGCTCGAGAGCTTTAA 848
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                                                 495 CIACITCACATCCCGCCACGGGATTAGCTTCACGGGTTACCGCTCCTAAAACATCTCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
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APPLICATION NUMBER: US 08/362,577
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY AGENT INFORMATION:
NAWE: Rin-Laures, Li-Heien
REGISTRATION NUMBER: 33,547
REFRENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION:
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,812
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60606-5402
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 20, Application US/08920812
; Patent No. 5763188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312/4
TELEX: 25-3856
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STREET: BOX
TWY. Chicago
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2211 PATRACTIGGCICATGAATCAGAAGGGGGCAGCCCTCCTCCGCCATGAACTCAGCGCCT 2270
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                                                           3028 CATICAATAAGTGTAGGCTGTTGAGGTTGGCTTCGGTAAGCATTTCGGCGTCAGGACCAC 3087
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                                                                                                                                 ------GCGGGAACCCTCTGGAATTCCATCGAGATATTTGT 2090
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GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Uchara, Akio
APPLICANT: Bda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3373 CGCATGAGCGAGAGAGAGGGGTTTCTTCCATCGGGGTATTT 3416
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STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-AUG-1997
CLASSIFICATION: 455
FILING DATE: 27-MAR-1995
FILING DATE: Z7-MAR-1995
ATTORNEY, GENT INFORMATION:
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REGISTRATUN NUMBER: 33.547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
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COUNTRY: United States of America
ZIP: 60606-6402
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; Patent No. 5798211
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: 312/474-0448
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STREET: 650
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                    APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTIONS: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60606-6402
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILIAG DATE: 29-AUG-1997
CLASSIFICATION: 435
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50.5%; Pred. No. 2.2e-19;
tive 0; Mismatches 332;
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REGISTRATION NUMBER: 33,547
REFERENCE, DOCKET NUMBER: 19036/32420
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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STRAIN: Clinical Isolate EC-625
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 5541 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.5
Matches 386; Conservative
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                 SENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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US-08-920-827-20
                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                   Length 5541;
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                                                                                                                     Query Match
4.2%; Score 100.8; DB 1;
Best Local Similarity 50.5%; Pred. No. 2.2e-19;
Matches 386; Conservative 0; Mismatches 332;
                                                   ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-625
           MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
linear
 TOPOLOGY:
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US-08-921-177-20
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Probe for Diagnosing Infectious Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                              3: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPATER: IBM PC compatible
COMPANIES PATEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 18/08/362,577C
PILING DATE: 27-NAR-1995
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    f.Match
Local Similarity 50.5%; Pred. No. 2.2e-19;
les 386; Conservative 0; Mismatches 332;
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19936/32420
                                                                         ADDRESSEE: Marshall, O'Toole, Gers
STREET: 6300 Sears Tower, 233 Sout
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6448
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Matches 386; Conservative
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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Sequence 20, Application US/08362577C Patent No. 5807673 GENERAL INFORMATION:

US-08-362-577C-20

APPLICANT: Ohno, Teuneya APPLICANT: Matsuhisa, Akio APPLICANT: Uehara, Hirotsugu APPLICANT: Eda, Soji

Pred. No. 2.2e-19;

50.5%;

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Best Local Similarity 50.5
Matches 386; Conservative
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                                                                                                                                                                                                                                        3313 TITGGICCGCTCIGGCGAGIAAGAGAGAICCCGACATAAACGCCTTACCGCTITGIA 3372
                                                                                     2151 CIGACIGCAACAAGTICTCACCGICAICGCCCGGIICCICCACCCAACGAITAAIGAIGG 2210
                                                 3148 cegickáckartechtskáckásásákarakásákárhatkasáckákesékaritkirtesk 3207
                                                                                                                                                                               3253 reracgaaderrgargaarraacaddddaarrrrccadroddddaddddadddarrr 3312
                    CCGTGAGCAGGCCCTGCGCAAGTGGTGAAAGCAATGACGCCAAGACCATTGTTGGCAG 2150
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APPLICANT: Ohno, Teuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Tehara, Hirotsugu
APPLICANT: Probe for Diagnosing Infectious Disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6066-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFMENTINE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
CLASSIFCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Rin-Laures, Li-Heien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/08920828
Patent No. 5853998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 5541 base pairs TYPE: mucleic acid STRANDEDNESS: double
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4.2%; Score 100.8; DB 2;

Query Match

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APPLICANT: GATY Breton et. al
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMOMIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREMOMIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US 609/409, 039A
CURRENT FILING DATE: 1099-01-29
RIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5370
LENGTH: 1095
TYPE: DNA
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Patent No. 6610836
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRAB
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERBURE: 2709,1002-001
FILE REPERBURE: 2709,1002-001
FILE REPERBURE: 2000-04-05
PRIOR PALICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
RECOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
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204 GGATCACTICTCCTGCTTTTAGCATGGGAGCAGCTTGGGGTTTCGGGAAGAAGTCCCCCAAC 263
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APPLICANT: GALY Breton et. al

APPLICANT: GALY Breton et. al

APPLICANT: GALY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.200401

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US/00-01-27

PRIOR PELING DATE: 1999-01-29

FRIOR FILING DATE: 1999-01-29
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUCINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
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Patent No. 6551795
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Pred. No. 3.2e-09;
0; Mismatches 453; Indels
PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 7644
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                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Lubbers, Mark W
APPLICANT: Lubbers, Mark W
APPLICANT: Lubbers, Mark W
APPLICANT: Lokker, James
TITLE OF INVENTION: Polymucleotides, materials incorporating
TITLE OF INVENTION: them, and methods for using them.
FILE REFERENCE: 104801
CURRENT PLILING DATE: 2000-11-28
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 124
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.7%; Score 64; DB 4; Length 1002;
Best Local Similarity 47.9%; Pred. No. 7.8e-09;
Matches 279; Conservative 0; Mismatches 270; Indels
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                               Sequence 24, Application US/09724623
Patent No. 6476209
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RESULT 14
US-09-724-623-24/c
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Sequence 7908, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al.

RESULT 15 US-09-252-991A-7908

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: 107196.136

CURRENT APPLICATION NUMBER: US 08/05/2,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 7908
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Best Local Similarity 54.6%; Pred, No. 2.9e-08;
Matches 148; Conservative 0; Mismatches 117;
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Job time: 198.837 secs
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US-09-252-991A-7908
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March 17, 2004, 00:51:03; Search time 851.071 Seconds (without alignments) 10269.549 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/US00 NEW PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 24, Appl	Sequence 1, Appli	Sequence 47, Appl	Sequence 3456, Ap	Sequence 51, Appl	Sequence 7, Appli	Sequence 3455, Ap	Sequence 9, Appli	Sequence 3454, Ap	Sequence 669, App	Sequence 17521, A	Sequence 17523, A	Sequence 35374, A	Sequence 38826, A	Sequence 38124, A
SUMMARIES	Q.I.	US-10-196-232-24	US-09-738-626-1	US-09-746-660A-47	US-09-738-626-3456	US-09-746-660A-51	US-10-166-142-7	US-09-738-626-3455	US-10-166-142-9	US-09-738-626-3454	US-10-627-476-669	US-10-282-122A-17521	US-10-282-122A-17523	US-10-369-493-35374	US-10-369-493-38826	US-10-369-493-38124
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d	Query Match	100.0	100.0	41.8	36.6	34.6	29.9	29.8	29.4	26.4	20.4	12.9	12.8	6.9	6.9	6.9
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Sequence 13437, A	Sequence 14749, A	Sequence 26429, A	Sequence 12, Appl	Sequence 12, Appl	Sequence 28444, A	Sequence 1110, Ap	Sequence 1, Appli	Sequence 11887, A	Sequence 1151, Ap	Sequence 1, Appli			19965,			Sequence 39389, A	Sequence 33379, A	Sequence 77, Appl	Sequence 1450, Ap	Sequence 6195, Ap	Sequence 20492, A	Sequence 12754, A	Sequence 41572, A	Sequence 23370, A	Sequence 1395, Ap	Sequence 41645, A	Sequence 9644, Ap	Sequence 40108, A	Sequence 38717, A
US-10-282-122A-13437		US-10-282-122A-26429	US-09-894-844-12	US-10-388-902-12	US-10-282-122A-28444		.4 US-10-156-761-1		כי	14 US-10-156-761-1			US-10-282-122A-19965	US-10-282-122A-7020				US-09-974-300-77	5 US-10-260-238-1450	US-09-815-242-6195			2 US-10-282-122A-41572	2 US-10-282-122A-23370	US-09-738-626-1395	2 US-10-282-122A-41645	US-09-815-242-9644	2 US-10-282-122A-40108	2 US-10-282-122A-38717
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ALIGNMENTS

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61 CCTGAACCTTTTCAGAAGTAACTAAGGCCGCAATCCCTCGATTGCTGCATCAACGACGGC
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    US-10-130-235-24

Squence 24, Application US/10196232

Publication No. US20030113899A1

GENERAL INFORMATION:
APPLICANT: YAMAGUCHI, MIKIKO
APPLICANT: TTO, HISAO
APPLICANT: TAGUEDA, HISASH
TITLE OF INVENTION: METHOD FOR PRODUCING L-ARGININE
TITLE OF INVENTION: METHOD FOR PRODUCING L-ARGININE
FILE REPERRANCE: 225391USO
CURRENT FILING DATE: 2002-07-17
CURRENT FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 2374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 2374; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Corynebacterium glutamicum
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Best Local Similarity 100.0
Matches 2374; Conservative
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
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US-10-196-232-24
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Qy	Qy 541 TAAAACATCTCCACGCCGCAGAAGATAATGTGTGCGCTTCATCTTCCAAGCGCAGCGT 600 bb 1329428 TAAAACATCTCCACGCGCAGCAAGAATAATGTGTGCGCTTCATCTTCCAAGCGCAGCGT 1329369 Qy 601 GAGCGTTGCTCCACCCCAAGAAGCTACCTCGTTGAACACGGGAAGGAA	Qy 721 TTTAGTTTCTGCAGCAACACCATTTTCCGCGCTGCACAGGACTTCACCCGC 780 Db 1329248 TTTAGTTCTGCTTGCAACAACACACTTTCCGCGCTGCTTGCACAAGGACTTCACCCGC 1329189 Qy 781 TTCGGTTGCTTTGGCCGGTTGCGCGCGATACCAACACCTCGACCTCACGTGATGCTCGAG 840 Db 1329188 TTCGGTTGCTTTGGCCGGTTGCGCGGATACCAACACTCGACCACGTGATGCTCGAG 1329129 Qy 641 AGCTTTAACGCGCTGACTCACCGCCGAGGGAAATGGAAACGCCACGTGATGCTCGAG 1329129 Qy 641 AGCTTTAACGCGCTGACTCACCGCCGAGGGAAATGGAAACGGCTTC 900			OY 1141 TCTCGTGTGTTTAATTTCTGACGTCTTTTTGTTCATCGCGGCACCTTGGGCGTTGATCT 1200 Db 1328828 TCTCGTGTGTTTAATTTCTGACGTCTTTTTTTTTTTTTCATCGCGGCACCTTGGGCGTTGATCT 1328769 OY 1201 TTTGTCCAATGCGGGGGGTCGTGTATTATGGGGTGGGTGG	1261 1328708 1321 1328648	1381 1328588 1441 1328528
Db 2281 CTCTGGACCGTAGGAAGAAATACCCACGTAAAGAGCCTTTCCAGACGCAACAATGTCACG 2340 Qy 2341 CAATGCGTACATGGTTCTTCCAAAGAGTATCT 2374 Db 2341 CAATGCGTACATGGTTTCTTCCAAAGAGTATCT 2374	SULT 2 Sequence 1 Sequence 1 Publication GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:	APPLICANT: TATEISHI, NAOKO APPLICANT: SENCH, AKHHRO APPLICANT: SENCH, MASATO APPLICANT: SENCH, MASATO TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REPERENCE: 249-125 CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-18 PRIOR FILING DATE: 1999-12-16 PRIOR PHILING DATE: 1999-12-16	ruurana	<pre>// ORGANISM: Corynebacterium glucamicum US-09-738-626-1 Query Match</pre>	DD 1329968 CCAITTGCTGAAGTGTTACTCTGCCCAATTCCTGCGGGGGGAAGAGAAAAC 1329909	Db 1329848 GTCTGTGAGTTGAGTTCTGAGTGAGTGAGTGAGTGAGTGA	Db 1329728 GGTTTCGGGAAAGTCCCCAACCAACCAACCTCGCCCAAAACCTCCGC 1329669

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AGCUTICCTCCACCCCAAGAAGCTACCTCGTTGAACACGGGAGGAAACCATGTGGATAGC 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACGGGACAATGGATACGCGCCTGCGCCCCACAGGACCATCGACGCCCCGTCCAGGTCA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GITICGGGAAGAAGICCCCCAAGGCCTCGGCGAATTGCCTCACCAAAACCTTCCGCC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      813 GTTTCGGGAAGAAGAAGTCCCCCAACCAAGGCCTCGGCGAATTGCCTCACCAAAACCTTCGGCC 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGTCTTGAAGCACATCTTTGGGACCGAAGCGTAAGACGGGCATCGCAGCCCAATCTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 TTCCCATCAACCATGTAGGCATCCCGCAATGAGGGGTTGCAATGGCCAAGTGGCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 573 GTICCAAGTTCTACTACATCCCGCCACGGGATTAGCTTCACGGGTTACCGCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 AAAACATCTCCACGCCGCAGCAAGGATAATGTGTGCGCTTCATCTTCCAAGCGCAGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 GITCCAAGITCTACTACTTCACATCCCGCCACGGGATTAGCTTCACGGGTTACCGCTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CP2
CURRENT APPLICATION NUMBER: US/09/746,660A
CURRENT FILING DATE: 2000-12-22
PRIOR PELICATION NUMBER: 09/603124
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 0/141031
PRIOR APPLICATION NUMBER: 60/141031
PRIOR PILING DATE: 1999-06-25
PRIOR PELICATION NUMBER: 60/142101
PRIOR PILING DATE: 1999-06-25
PRIOR PELICATION NUMBER: 60/14613
PRIOR PILING DATE: 1999-00-12
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: RXA01393
US-09-746-660A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
APPLICANT: Kim, Jun-Won
APPLICANT: Liee, Heung-Schick
APPLICANT: Hwang, Byung-Joon
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APPLICANT: Pompejue, Markus
APPLICANT: Schroder, Burkhard
APPLICANT: Schroder, Burkhard
APPLICANT: Schroder, Barwig
APPLICANT: Alberhauer, Gregor
APPLICANT: Kim, Jun-Won
APPLICANT: Head, Heung-Schick
APPLICANT: Head, Byung-Joon
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: WATABOLIC PATHWAY PROTEINS
FILE REPERENCE: BG1-12.1CP2
CURRENT APPLICATION NUMBER: US/09/746,660A
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US-09-746-660A-51
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                                                                                                                            TTAGTTTCTGCTTGCAGCAACACCATTTTCCGCGCTGCTTGCACAAGGACTTCACCCGGCT 781
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            AGCGTTGCTCCACCCCAAGAAGCTACCTCGTTGAACACGGGAGGAAACCATGTGGATAGC 394
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Sequence 3456, Application US/09738626

Publication No. US20020197605A1

GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NAKAGHI, MIKIRO
APPLICANT: NAKOSHI, MIKIRO
APPLICANT: TANESHI, NACKO
APPLICANT: TANEISHI, NACKO
APPLICANT: TANEISHI, NACKO
APPLICANT: TANEISHI, NACKO
APPLICANT: TANEISHI, NACKO
APPLICANT: SENOH, AKHHIRO
APPLICANT: SENOH, AKHHIRO
APPLICANT: SENOH, AKHHIRO
APPLICANT: 1KEDA, MASATO
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CURRENT FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEO ID NO 4456
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US-09-738-626-3456
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Sequence 7, Application US/10166142

| Sequence 7, Application US/10166142
| Publication No. US20030124667A1
| GENERAL INCRAMATION NO. US20030124667A1
| GENERAL INCRAMATION NO. USABLIA
| APPLICANT: GUNIT, YOSHIYA
| APPLICANT: YASUEDA, HISASHI
| TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL FILE REFERENCE: 223789US
| CURRENT APPLICATION NUMBER: US/10/166,142
| CURRENT APPLICATION NUMBER: DP 2001-1777075
| PRIOR FILING DATE: 2002-06-11
| PRIOR FILING DATE: 2001-06-12
| NUMBER OF SEQ ID NOS: 10
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 7
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601 CGGCGCGCAATACGGCGACACCGGACGGTGTTTTCGCCGCTGGCGCGTTCGCGGCAAG 660
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                                                                                                                            1585 CCTGATCTGGTTCCCGCTGGTTTCGGCGCAGCAGCATTGTCACGCCCGCTGTCCAG
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                                                                                                                                                                                                           Query Match 29.9%; Score 711; DB 14; Best Local Similarity 100.0%; Pred. No. 1e-226; Matches 711; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Brevibacterium lactofermentum
FEATURE:
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US-10-166-142-7
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34.6%; Score 822; DB 10; Length 822;
Best Local Similarity 100.0%; Pred. No. 7.1e-264;
Matches 822; Conservative 0; Mismatches 0; Indels
               PRIOR FILING DATE: 2000-12-22
PRIOR PELING DATE: 2000-06-23
PRIOR PLING DATE: 2000-06-23
PRIOR PELING DATE: 2000-06-23
PRIOR PELING DATE: 2000-06-23
PRIOR PELING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141031
PRIOR APPLICATION NUMBER: 60/142101
PRIOR APPLICATION NUMBER: 60/142101
PRIOR APPLICATION NUMBER: 60/148613
PRIOR APPLICATION NUMBER: 60/18970
PRIOR PELING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/18970
PRIOR PELING DATE: 1999-00-30
PRIOR PELING DATE: 1990-00-30
PRIOR PELING DATE: 1990-00-30
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR PELING DATE: 1990-07-08
                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (101)..(799)
; OTHER INFORMATION: RXA01394
US-09-746-660A-51
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
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LENGTH: 822
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Qy 1256 TACCTGTTATGGTTTGCGTCATGGCAGCGAAAGACGCCATGACAAACAA	0y 1556 ATTITICGCCGCTGGCCGCAAGCCTGATCTGCTTCCGCTGGTGGGTTCGGC 1615	RESULT 8 US-10-166-142-9 US-10-166-142-9 Sequence 9, Application US/10166142 Publication No. US20030124687A1 GENERAL INFORMATION: APPLICANT: VASUEAN: HISASHI TITLE OF INVENTION: METHOD PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL TITLE OF INVENTION: MASSIMILATING BACTERIUM FILE REFERENCE: 223789US CURRENT APPLICATION NUMBER: 2002-06-11 PRIOR APPLICATION NUMBER: J010-06-12 CURRENT FILING DATE: 2001-06-12 NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin version 3.1 EMOTH: 712 TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA	; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)(375) ; OTHER INFORMATION: US-10-166-142-9	Query Match 29.4%; Score 696.8; DB 14; Length 712; Best Local Similarity 99.6%; Pred. No. 5.7e-222; Indels 1; Gaps 1; Matches 709; Conservative 0; Mismatches 2; Indels 1; Gaps 1; Qy 1016 ATGGTGATCATGGAATCTTCATTACAGGTCTGCTTTTGGGGCCAGTCTTTTGCTGTC 60 Qy 1076 ATCGGACCGCAGAATCTTCATTACAGGTCTGCTTTTTGCTGTC 60 Db 61 ATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGGAAGGACTCATTGCTGTC 6135 CQy 1136 GTTCTTCTCGTGTGTTTAATTACTGACGTCTTTTTGTTCATCGCCGAAGGACTCATTGCG 120
Qy 1436 GTTTGGGTAAAGCCCATGTTGATGGCAATGGTGACCTGGTTGAACCCGAATGGTAT 1495 Db 421 GTTTGGGTAAAGCCCATGTTGATGGCAATGGTGACCTGGTTGAACCCGAATGCGTAT 480 Qy 1496 TTGGACCGTTTGTGTTTATCGGCGGCGCGCGCAATACGGCGACCCGGACGGTGG 1555 Db 481 TTGGACCGTTTGTGTTTATCGGCGGCGCGCAATACGGCGACACCGGACGGTGG 540 Qy 1556 ATTTTGGCCGTTTGGCGGTTCGCGGCGCAAGCTGATCCGGTGGTGGGGGTTTCGGC 1615 Db 541 ATTTTGGCCGTTGGCGGCTTCGCGGCAAGCCTGATCTGGTTCCGCTGGTGGGGTTTCGGC 600 Qy 1616 GCAGCAGTTGTCACGCGCTGTCCAGCCCCAAGGTGTGGCGTGGATCACGTCGTC 660 Qy 1676 GTGGCAGTTGTCACGCCTGTCCAGCCCCAAGGTTGGCGTTGATCACTCGTC 660 Qy 1676 GTGGCAGTTGTCACGCCTGTCCAGCCCCAAGGTTGGCGTTGATCACTCGTC 660 Qy 1676 GTGGCAGTTGTGATGACCCCAAGGTTGATGATGTTGATGACTTGATCGTC 660 Db 601 GTGGCAGTTGTGATGACCCCCAAGGTTGATGATGATGATGATTGAT	RESULT 7 US-09-738-626-3455 ; Sequence 3455, Application US/09738626 ; Publication No. US20020197605A1 ; GENERAL INFORMATION: ; APPLICANT: NAXBARM, SATOSHI ; APPLICANT: MAXBARM, SATOSHI ; APPLICANT: HAYSHI, HIROSHI ; APPLICANT: HAYSHI, MIKIRO ; APPLICANT: HAYSHI, KEIKO ; APPLICANT: YOKOL, HARUHIKO	APPLICANT: TATEISHI, NAGKO APPLICANT: SENOH, AKHHRO APPLICANT: SENOH, AKHHRO APPLICANT: SENOH, AKHRO TITLE CANKI, AKI CONKI, AKI FILE REPERBNCE: 249-125 CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT PAPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 1999-12-16 PRIOR APPLICATION NUMBER: US/05/162 PRIOR APPLICATION NUMBER: US/05/162 PRIOR APPLICATION NUMBER: US/05/162 PRIOR APPLICATION NUMBER: US/05/162 PRIOR FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7069 SQCTWARE: Patentin ver: 3.0 SCTWARE: Patentin ver: 3.0 STQ ID NO 3455 LENGTH: 708 TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA US-09-738-626-3455	Query Match 29.8%; Score 708; DB 9; Length 708; Best Local Similarity 100.0%; Pred. No. 1e-225; Matches 708; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ON 1016 ATGGRACATGGAAATCTTCATTAGAGGTCTGCTTTTGGGGGCCAGTCTTTTAGGGCGCA	1076 ATCGGACCGCAGAATCTTCATTACAGGTCTGCTTTTGGGGGCCCAGTCTTTACTGTCC 1076 ATCGGACCGCAGAATCTTCATTACAGGTCTGCTTTTGGGGGCCCAGTCTTTTACTGTCC 1076 ATCGGACCGCAGAATGTACTGGTGATTAAACAAGAATTAAGCGCGAAGGACTCATTGCG 1136 GTTCTTCTCGTGTGTTTAATTTCTGACGTCTTTTTGTTCATCGCCGGCACCTTGGGGTT 121 GTTCTTCTCGTGTGTTTAATTTCTGACGTCTTTTTGTTCATCGCCGGCACCTTGGGGGTT 1196 GATCTTTGTCCAATGCCGCGCCGATCGTGCTTTTTTTTTT

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APPLICANT: Kroger, Burkhard
APPLICANT: Kroger, Burkhard
APPLICANT: Schoder, Burkhard
APPLICANT: Schoder, Burkhard
APPLICANT: Schoder, Burkhard
APPLICANT: Abberhauer, Gregor
TITLE OF INVENTION: CORNEBBATERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: CORNEBBATE INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BG1-125CPCN
CURRENT PILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: 09/602,787
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
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                                                                                                              1726 GITTICGCGGGTITTIGGAATCGGTGGCCTTCGCCCAAATGTTGATGCCGGCGTCGTGGGA
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0
    Length 627
                                          Indels
Query Match 26.4%; Score 627; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.3e-198;
Matches 627; Conservative 0; Mismatches 0;
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US-10-677-476-669/c
; Sequence 669, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
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                                                                                                                                                         1316 CCACAGATCATTGAAGAAACAGAACCAACCGTGCCCGATGACACGCCTTTGGGCG-GTTC 1374
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                                                                         GATCTTTTGTCCAATGCCGCGCGCATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCT 1255
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APPLICANT: ANDO, SELKO
APPLICANT: ANDO, SELKO
APPLICANT: CHIAL, KELKO
APPLICANT: COCTIAL, KELKO
APPLICANT: TATELEHI, NAOKO
APPLICANT: TREEBHI, NAOKO
APPLICANT: TREEBHI, NAOKO
APPLICANT: TREEBHI, NAOKO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
APPLICANT: 0ZAKI, AKIO
APPLICANTON: NUMBER: US/09/738,626
CURRENT FILING DATE: 1090-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR PLING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3454, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZCGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin ver. 3.0
SEQ ID NO 3454
LENGTH: 627
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SEQ ID NO 17521
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PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PELING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
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Pred. No. 5.8e-151;
0; Mismatches 3; Indels
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US-10-283-122A-17521/c
Sequence 17521, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: DE 19931563.9
                                                                                                                                                                                                                                                                                                                           ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 20.4%;
Best Local Similarity 99.0%;
Matches 499; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (101)..(970)
; OTHER INFORMATION: RXN03164
US-10-627-476-669
                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
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APPLICANT: Wang, Liangsu APPLICANT: Zamudio, Carlos APPLICANT: Malone, Cheryl

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2090 TCCGTGAGCAGGCCCTGCGCAAGTGGTGAGAAAGCAATGACGCCAAGACCATTGTTGGCA 2149
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                                                                                           APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Yamandro, Robert
APPLICANT: Foresyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLICATION NUMBER: 60/191,078
PRIOR PLILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-05-3
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-66
PRIOR PLILING DATE: 2000-09-06
PRIOR PLILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-11-27
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PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2001-12-22
PRIOR PLILING DATE: 2001-02-22
PRIOR PLILING DATE: 2001-02-26
PRIOR PLILING DATE: 2001-02-26
PRIOR PLILING DATE: 2001-02-26
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Best Local Similarity 67.1%;
Matches 433; Conservative
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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US-10-369-493-35374/c
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APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Will H.
TITLE OF INVESTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA. 034A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/235,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-26
PRIOR PILING DATE: 2001-02-26
PRIOR PILING DATE: 2001-02-26
PRIOR PILING DATE: 2001-02-26
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
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PRIOR PILING DATE: 2001-02-16
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GCTGACTGCAACAAGTTCTCACCGTCATCGCCCGGTTCCTCCACCCAACGATTAATGATG 2209
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                                                                                                                                                                                                                                           Sequence 17523, Application US/10282122A
Publication No. US20040029129A1
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US-10-282-122A-17523
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APPLICANT: Zamdio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeelbeck, Robert
APPLICANT: Ohlsen, Kari
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Best Local Similarity 59.2%
Matches 517; Conservative
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Wall, Daniel
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Carr, Grant
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APPLICANT:
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfen
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION C
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVARTION: EXERSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVARTION: PEARNS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)
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Pred. No. 1.8e-43;
0; Mismatches 236;
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CURRENT APPLICATION NUMBER: US/10/369,493
                        CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                                                                                           ) ORGANISM: Agrobacterium tumefaciens US-10-369-493-38826
                                                                                                                                                                                                                                                                                                                6.9%;
                                                                                                      NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 38826
LENGTH: 1026
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Matches 359; Conservative
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                                                                                                                                                                                                   TYPE: DNA
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Gldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)
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CURRENT APPLICATION NUMBER: US/10/369,493
                     CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                           ; ORGANISM: Agrobacterium tumefaciens US-10-369-493-35374
                                                                                                                                                                                                                                                                                                                   Query Match 6.9%;
Best Local Similarity 57.2%;
Matches 359; Conservative
                                                                                                         NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 35374
LENGTH: 1026
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-1
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 38124
LENGTH: 1028
                                                                                                           ; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38124
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Torres-Jerez, L., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tagg from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library

Unpublished (2001)
Contact: May GD Plant Biology Division
The Samuel Roberts Noble Foundation
7510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
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Email: gdmay@noble.org
BZ554294 pacs1-60
BZ556569 pacs2-164
BZ55695 pacs2-164
BZ55695 pacs1-60
AL108460 Drosophil
BX355695 pacs1-60
AL2059021 1117004E0
CD881613 F1.103123
GA8229022 1114036D0
BX391661 BX391687
BX381961 BX381961
AL24706 P4610C04
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AL24709 Pacs2-164
BZ552255 pacs2-164
BZ574094 msb2 3.50
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BX435603 BX424625
BX435897 CSJNEG10
BX361080 BX361080
CB66977 OSJNEG108
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CA17225 SCCCLEZ20
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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermaryota, Viridiplantae, Streptophyta; Embryophyta, Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                CA830247
CD881613
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BQ704105
CNS037K47
BX361961
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CB668778
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                                                                              March 15, 2004, 13:43:00; Search time 6528.5 Seconds (without alignments) 10858.975 Million cell updates/sec
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                                                                                                                                                     1 ccatttgctgaaggtgttac......tttcttccaaaggagtatct 2374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                     55026578
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                             27513289 seqs, 14931090276 residues
                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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BH770958
AF075981
CNS01MQH
                                                             nucleic search, using sw model
                                                                                                                                                                           IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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em_gss_nun:..
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em_gss_pto:..
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em_gss_vr1:..
em_gss_vr1:..
ep_gss_vr1:..
                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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28
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2374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.6
73.2
72
60.4
                                                                                                                                            Perfect score:
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source

FEATURES

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2193 TRATGAGGATCACGCATTCGCGAATTTTCAGGAATTCCATGCAAATATTTTCCTGTTAAG 2252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2159 AACAAGTICTCACCGICAICGCCCGGTICCTCCACCCAACGATTAATGATGGAATAGCTT 2218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2296 cccrcrcricaaagrrricrigraaarcarcrricaarccarccarcaacarraacarraacaa 2355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2356 GGCIGATGAATCAAGACTTTAAAGCCTAACTTTTCAGCCGCTAAGACCGCAGCTTCGGTT 2415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1805 AACTCGGGGTCAGAAAACTCCAAGTTGTTGAGTGAATCAAGGCTGTTGTCCAGCTGCTCA 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2073 CGTAAAACCCAAGCTTATGCCATTTGAGCTAGAGATTGTCCACGACTTTGAGCTAAATCA 2132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2219 GGCTGATGAATCAGAAGCGGGCAGCCCTCCTCCGCCATGAACTCAGCCGCCTCCGCTGTG 2278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1865 ACTGACGAAGCACCAATGAATGCACTGGTCACGGTATCCGCGCCGTACTCTCCTTGCTCG 1924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2045 CCCTGGCTGGCGCGG-----GAACCCTCTGGAATTCCATCGAGATATTTGTCCGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                               Domaine de Vilvert, 78352 Jouy en Josas cedex, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2016 GGACGACTTGCCCCAATCAAAGCTGAACAACTTGAACTTTGCCAGCTCTT---TCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2133 TIAAGGGCTIGAACTIGITCCAAICTITCIGIGGIAAGACTGICAICAIGAAAGICGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db xref="textor:1359" Sequence Tag Library" //olone lib="MG1363 Random Sequence Tag Library of //olone="vector: pSGMU2; Site 1: Smal; Library of chromosomal fragments of Liactis strain MG1363 was prepared by partial AluI digestion or by sonication."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1956 AATTCTTCGTCAGTAAATTCCAGACGTTCTAAAGCTGCAACATTTTCAATGATTTGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1925 CGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGGCGTTCCTGGGCGATGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1985 ITGAGCTTGCGGACCATATCAATATTGTTCACGTTCAACATGCCCTCAGACAGGGACTTA
                                                                                                                                      Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                           Bolotin, A., Ehrlich, S.D. and Sorokin, A. Studies of genomes of dairy bacteria Lactococcus lactis Sci. Aliments (2002) In press Contact: Sorokin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Lactococcus lactis subsp. cremoris"
/mol_type="genomic DNA"
/strain="MG1363"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 73.2; DB 28; Length 3 Pred. No. 9.5e-08; 0; Mismatches 263; Indels
cremoris genomic, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2253 AGTCCTTGATACAAAGGCTTAAAGGCAATTGTTCCTATCCC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             best homologue in strain IL1403 is nadR (98%)
                                                                                                              Lactococcus lactis subsp. cremoris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8top: 3207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sub species="cremoris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence start: 30
High quality sequence stop: 3207
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: sorokine@jouy.inra.fr
                                                    BH770958.1 GI:20373915
                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
                                                                                                                                                                                                                                                                                                                                                             Genetique Microbienne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.1%;
Similarity 49.8%;
                                                                                                                                                                                                                          (bases 1 to 3237)
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                                                                                                                                                                                                   Lactococcus.
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                                                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
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                                                                                                                                                                                                                                                                                                         /dow_scape specialists
/clone_lib="Intradiated"
/note="Wector: Lambda Zap; Seedlings were exposed either
to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
poly4+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-ZAP XR vector using ExAssist
// Alphor phage and the E. coll strain XII-blue NRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH770958 3237 bp DNA linear GSS 01-MAY-2002 LLMGtag686 MG1363 Random Sequence Tag Library Lactococcus lactis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTCCAAGCGCAGCGTGAGCGTTGCTCCACCCCAAGAAGCTACCTCGTTGAACACGGGA 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          644 GGAAACCATGTGGATAGCGAATCTGCGTTGATGGCGATGGTTAACGGGATTTCAGCAAGG 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 ATGGCCAAGTGGCGCATGGTTCCAAGTTCTACTTCACATCCCGCCACGGGATTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  524 TCACGGGTTACCGCTCCTAAAACATCTCCACGCCGCAGCAAGGATAATGTGTGCGCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 TCTTCTACCTGCAAGTTGAGGCGGATAGGCGAATCAGCCAACACAGGAGCCAGTGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 ACGAACAGATAGTCGAGCGCCACCAAGTTTATCGACAAGACAACTCGGCAGCGCCTGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         704 CGTCCAGATAGTIGCGCTTTAGTTTCTGCTTGCAGCAACACCATTTTCCGCGCTGCTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 84.6; DB 13; Length 657;
Pred. No. 3.4e-11;
0; Mismatches 255; Indels 0;
                                                                                                                                              organism="Medicago truncatula"
           Std Error: 0.00
                                  Plate: 075 row: E column: 08
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                             tissue type="seedlings"
                                                                                                                                                                                                      'db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                          'dev stage="seedling"
                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                   clone="NF075E08IR'
                                                                                                                                                                           mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.6%;
Best Local Similarity 48.2%;
Matches 237; Conservative
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           Insert Length: 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1218 CGATCCTGCTCGATATTATGCCGCTGGCATCGCTTACCTGTTATGGTTTGCCGTCA 1277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope.

Direct Submission

Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BPP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr )

C (bases 1 to 830)

Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J. Direct Submission

Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1098 TGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCGGTTCTTCTCGTGTTTTAATTT 1157
                                                                                                                                                      GSS 14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537 idaigaarcagedearceccecceccarcrearcarisecciecrareceras 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477 gidarrigciecricarcrendecedaarrirrigdeedageageargeagrendargeagrene 418
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                                                                                                                                                      CNSOIMOH Anopheles gambiae GSS T7 end of clone 22E24 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597 KTCAAGGCCTTGCCTTAGGTGCATTTTTTTTTTTTCCCCTCGGCCCGCAAAATGCGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1158 CTGACGTCTTTTTGTTCATCGCCGCCACCTTGGCGTTGATCTTTTGTCCAATGCCGCGC
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                                                                                                                                                                                                                                                                                                                                                               Bukāryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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2282 TCTGGACCGTAGGAAGAATACCCACGTAAAGAGCCTTTCCA 2323
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                       318
                                                                                                                                                                                                                                                                                                                 Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
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/mol_type="genomic DNA"
/strain="PEST"
/db_xref="text"
/clone="22E4"
/clone_lib="NotreDame1"
/note="end : T?"
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/organism="Anopheles
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AL151258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1985 ITGAGCTTGCGGACCATATCAATATTGTTCACGTTCAACATGCCCTCAGACAGGGACTTA 2044
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                                                                                                                                                                                                                              AF075981 GSS 29-AUG-2000 AF075981 Salmonella typhimurium LT2, Lambda DASH II Salmonella typhimurium genomic clone 390-T3, genomic survey sequence.
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  2416 TCTTTGGCAGAATAATTAGACAAACCCACATAAAGTGCTTTTCCACTATCCAGAGCAGTT 2475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 CTTCCGCTCGCCGCGCGGGAATCTTCCGGAATACCATTCAAATTACGGTCAGTGAGC-TG 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----cccgrccrcraccaacccrcaaaaccaararrraggc 120
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                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
1 (bases 1 to 860)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wong, R.M.-Y., Wong, K.K., Benson, N.R. and McClelland, M.
Sample sequencing of a Salmonella typhimurium LT2 lambda library:
comparison to the Escherichia coli KI2 genome
FEMS Microbiol. Lett. 173 (2), 411-423 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lambda DASH II"
| using Li-Cor
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/clone lib="Salmonella typhimurium LT2, Lambda
/note="Vector: Lambda DASH II, sequenced using
sequencer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3099 Science Park Road, San Diego, CA 92121, USA
Email: mcclelland@lifsci.sdsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Salmonella typhimurium"
|mol_type="genomic DNA"
|strain="LT2"
                                                                       2339 CGCAATGCGTACATGGTTTCTTCCAAAGGAGTATCT 2374
                                                                                                      2476 TTCAAAGCGCCCAIGGTTTCTTCAATAGGGGTATTT 2511
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Sidney Kimmel Cancer Center
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Matches 220;
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AF075981/c
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Matches 143; Conservative
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Pseudomonas aeruginosa
Bacteria, Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 897)
                                                                                                                                                                                                                                                                                                                                        Pseudomonadaceae; Pseudomonas.

1 (bases 1 to 1034)

Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Supencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Surns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
    pacs1-60_4617.x1 pacs1-60 Pseudomonas aeruginosa genomic clone
pacs1-60_4617, genomic survey sequence.
BZ554294.1 GI:27161466
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/clone="pacs1-60 4617"
/clone=lib="pacs1-60"
/clone=lib="pacs1-60"
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/strain="1-60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 2066857244
Email: craymond@u.washington.edu
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Location/Qualifiers
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Tel: 2062216954
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BZ568946 165.y2 pacs2-164 Pseudomonas aeruginosa genomic clone pacs2-164 8165.y2 pacs2-164 Pseudomonas aeruginosa genomic clone pacs2-164_8165, genomic survey sequence.
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Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Bredomonas aeruginosa library
J. Bacteriol. (2002) In press
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V. Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
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/clone lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library."
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Pred. No. 0.0067;
0; Mismatches 120; Indels
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University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
                                                                                                                                                                                                                               Box 352145, Seattle, WA 98105-2145, USA Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1695 CATTGGCCATCAAACTGATGTTGATGGGTTA 1725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="2-164"
/db_xref="taxon:287"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Pseudomonas
                                                                                                                       J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                   Genome Center
University of Washington
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BZ568946.1 GI:27202770
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                                                                                                                                        1492 GTATTTGGACGCGTTTGTGTTTTATCGGCGCGTCGGCGCGAATACGGCGACACCGGACG 1551
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1732 GCGGGTTTTGGAATCGGTGGCCTTCGCCCAAATGTTGATGCCGGCGTCGTCGGGAAATCTC 1791
                                                                                                                                                                                                                                                                              1612 CGGCGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGT 1671
                                                                                                                                                                                                                                                                                                                                                               1672 CGTCGTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATGGGTTAGTTTTC 1731
                                                                                                                                                                                                                                                                                                                                                                                         Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                        pacs1-60_5975.x1 pacs1-60 Pseudomonas aeruginosa genomic clone
pacs1-60_5975, genomic survey sequence.
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/clone="pacs1-60"
/clone=lib="pacs1-60"
/note="clinical isolate 1-60 Whole genomic shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                              2.1%; Score 48.8; DB 29; Length ilarity 14.5%; Pred. No. 0.21; Conservative 156; Mismatches 121; Indels
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University of Mashington
Box 352145, Seattle, WA 98105-2145,
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/strain="1-60"
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779 GBCSSTGGCSCCCYCSTCSTC 756
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Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: shotgun.
                                                      Best Local Similarity
Matches 47; Conserv
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- Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EGGP) - http://www.edgp.bhi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBACII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS017SY 1101 bp DNA linear GSS 26-UUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37LO8 of DrosbAC library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                           1542 ACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGC 1601
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterayota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                         /db.xref="taxon:287"
/clone="pace2-164 8165"
/clone="bace2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library."
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                                                                                                                                                                                                                                                                                                           Score 51.4; DB 28; Length 1620;
Pred. No. 0.052;
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                 /organism="Pseudomonas aeruginosa"
/mol_type="genomic_DNA"
/strain="2-164"
                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
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/clone lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
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AL108460
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Matches 100; Conservative
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1038 TTACAGGICTGCTTTTGGGGGCCAGTCTTTTACTGTCCATCGGACCGCAGAATGTACTGG 1097
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                                                                                                                                                       1520 GECGICGECGCAAIACGGCCGACACGGIGGAITITICGCCGCTGGCGTTCGCG 1579
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                                                                                                                                                                                                        151 SSYSSSTCSCCTCCCSYSYSSSTSSSSSTSWGSTSGSSSSSVGTSSSSDSTSTCCSCCY 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX393687 Homo sapiens NEUROBLASTOWA COT 25-NORWALIZED Homo sapiens
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Genescope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODCOOLADO4QFI.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Li, M.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001).
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ilarity 17.2%; Pred. No. 0.4;
Conservative 152; Mismatches 178;
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/db_xref="taxon:9606"
/clone="CS0DC001YG07"
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Drosophila melanogaster genome survey sequence TBT3 end of BAC #BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
1067 TTACTGTCCATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAGGA 1126
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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Location/Qualifiers
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1 Similarity 13.8%; Pred. No. 0.22;
49; Conservative 157; Mismatches 149;
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Drosophila melanogaster
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/db_xref="taxon:7227"
/clone="BACR19D16"
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AL053013
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/note="end : TET3"
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CD881613 720 bp mRNA linear EST 14-JUL-2003 F1.103123F010329 F1 Triticum aestivum cDNA clone F1103123, mRNA
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1544 ACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTG 1603
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 720)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoplante, a major partnership french program in plant genomics Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93, rue Henri Rochefort 91025 EVRY CEDEX France
121: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
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Pred. No. 0.98;
0; Mismatches 140; Indels
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clone lib="F1"
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/clone="F1103L23"
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/cultivar="recital"
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larity 48.1%;
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TITLE
JOURNAL
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CD881613
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KEYWORDS
SOURCE
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                                                                                                   1278 ---TGGCAGCGAAAGACGCCATGACAAACAAGGTGGAAGCGCCACAGATCATTGAAGAAA 1334
                                                                                                                                                                                                                              CAGAACCAACCGTGCCCGATGACACGCCTTTGGGCGGTTCGGCGGTGGCCACTGACACGC 1394
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                                                                                                                                        621 KITIKKKKKINKAMMIKANMMIKGAMMOGGAMMGGAMMGGAMMGGAMMGGAMM 680
                                                                                                                                                                                                                                                               /clone lib_"1117 - Unigene V from Maize Genome Project"
/note="This library represents the unique genes found in
the fifth round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
library 946. Contigs were assembled using ZmDBAssembler
and 2 representatives from each contig were selected for
the Unigene set. All singlets were also selected."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, FACCAD clade, Panicoideae, Andropogoneae, Zea.
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Pred. No. 0.9;
0; Mismatches 175; Indels
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855 California Ave, Palo Alto, CA 94304, USA
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/mol_type="mRNA"
/db_xref="dbsST:946110C04.y1"
/db_xref="taxon:4577"
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Department of Biological Sciences
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Plate: 1117004 row: E column:
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Conservative 0;
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Fax: 650 725 8221
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/note="Organ: tassels, Vector: HybriZAP, Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the CDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
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BQ704105 644 bp mRNA linear EST 16-JUL-2002 946110004.y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 644)
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/lab_host="XLOLR"
/lab_host="XLOLR"
/lol_lib="946 - tassel primordium prepared by Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize ESTs from various cDNA libraries sequenced at Stanford
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Fax: 650 725 8221
Email: walbot@stanford.edu
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                                                                                                                   CA829022 620 bp mRNA linear EST 11-DEC-2002
1114036D07.y2 1114 - Unigene IV from Maize Genome Project Zea mays
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/mol_type="mENA"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone lib="lil4 - Unigene IV from Maize Genome Project"
/note="This library represents the unique genes found in the fourth round of EST sequencing at Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for the maize genome project. Sequences are present from libraries 1091 and 3524. Contigs were assembled using EmbBasembler and 2 representatives from each contig were selected for the Unigene set. All singlets were also selected."
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1.9%; Score 44.4; DB 14; Length 620;
Best Local Similarity 46.0%; Pred. No. 2.5;
Matches 150; Conservative 0; Mismatches 176; Indels 0.
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Department of Biological Sciences
Stanford University
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Fax: 650 725 8221
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Gaps

Search completed: March 16, 2004, 02:52:12

RESULT 15 BQ704105/c

Job time : 6533.5 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nuc	OM nucleic - nucleic search, using sw model	
Run on:	<pre>March 15, 2004, 10:15:20 ; Search time 2846.7 Seconds (without alignments) 10825.501 Million cell updates/sec</pre>	Đ
Title: Perfect score: Sequence:	US-09-105-117K-1_COPY_1016_1726 711 1 atggtgatcatggaaatcttaactgatgttgatgggttag 711	
Scoring table:	IDENTITY NUC Gapext 1.0	
Searched:	3470272 segs, 21671516995 residues	
Total number of	Total number of hits satisfying chosen parameters: 6940544	
Minimum DB seq : Maximum DB seq]	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AX643028 Sequence AX063712 Sequence AX064713 Sequence XX044059 Sequence XX244059 Sequence AX12419 Sequence BX16565 Novel BX16565 Novel BX16565 Novel BX16565 Novel BX16565 Novel BX16483133 Corynebac AX64030 Sequence BX248357 Corynebac AX640518 Sequence BX248357 Corynebac AX640518 Corynebac AX640518 Sequence BX248357 Corynebac AX016485 Sequence BX164059 Sequence BX164059 Streptomy AE016313 Streptomy AE016313 Streptomy AE016312 Shewanell AE01632 Streptomy AE016312 Shewanell AE01636 Shigella AE01636 Shigella AE016312 Shewanell AE01631 Sarcherich AE01664 Salmonell AE01664 Salmonell AE01664 Salmonell AE016727 Salmonell AE016727 Salmonell AE01676 Sequence AX1445 Escherichia AC145927 Gallus ga AL64607 Ralstonia AE01736 Sequence AX64607 Ralstonia AE01736 Sequence AX64607 Ralstonia AE01736 Sequence BX248341 Mycobacter BX848757 Sequence AX387945 Sequence	11 bp DNA linear PAT 24-FEB-2003 [266966. n Actinobacteridae; Actinomycetales; bacteriaceae; Corynebacterium.
SUMMARIES	AX643028 AX66371 AX244059 CGUXSEG A93333 AP005277 AX123539 BD165656 BX123539 BD165656 BX123539 BD165656 BX123539 BX105277 AE01572 AE01677 AE01677 AE01677 AE01677 AE016871 AE016871 AE016871 AE016871 AE015227 AE016871 AE01526 AE01526 AE01526 AE01526 AE01526 AE01530 AE01530 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE012410 AE015394 AE015394 AE015394 AE015394	nt EP1 158 amicur amicur eria; orynel 'H.
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Result No. Score	00 00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 AX643028 LOCUS DEFINITION ACCESSION ACCESSION KEYWORDS SOURCE ORGANISM TITLE
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/note="unnamed protein product; RXA01394"
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Sequence 53 from Patent WO0100843.
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LDAFVFIGGGGAQYGGTGRWIFPAGAFFAASLIWFPLVGFGAALSRPLSSFRVWRWIN
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                                                                             /organism="Corynebacterium glutamicum"
/mol_type="unassigned DNA"
/db_xref="taxon:1718"
1. 711
                                                                                                                                                                                                    /note="unnamed protein product"
/codon start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                        db_xref="REMTREMBL:CAD67811"
Patent: EP 1266966-A 7 18-DEC-2002;
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/db_xref="G1:28550159"
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Location/Qualifiers
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                                                                                 TIGGACGCGTTIGIGITITATCGGCGCGTCGGCGCGCAATACGGCGACACCGGACGGTGG
                                                                                                                               541 ATTTTCGCCGCTGGCGCGTTCGCGGCCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGC
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/mol_type="unassigned DNA"
/db_xref="taxon:1718"
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PSYSINRWYERPGDGENLLQSAANNGLGYATSPILAGGLITDKYLDGIPEGSRASQ
GKSLSEGMINNNIDWRKINDAQERGOSLAQMALAWYLREGESYGADIYTSALIGA
SKYRQLDNRLDSLNNILEFSDAELFAIDEISHHDGINWAKTDSKTREN"
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                                                                           RVLVSRTQPAKATEAGEVLVQAARKOVILQAETKAQLSGRLAEIPLTIAINADSLSTW
FPPVEVREVASWGGATLTLAILEDBATLTSLITREODVLGAVTEANVYGAGGEVVELGTRR
HLALATPSLINGAYWOGKLDAAMAVILREGPKOVLQDRDLIDGRVDGVGRRVSIVDS
AEGFGEAIRRGLGWGLLPETQAAPMIKAGEVILLDEIPIDTPWYWQRWRLESRSLARL
                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MEIFITGLLLGASILLSIGPQNVLVIKQGIKREGLIAVLLVCLI
SDVFFIAGYDLGADLLSNAAFILDIKWGGTAYLLMFAKAAKDAMTKVBARQIIE
ETEPTVEDDTELGGSAVATDTRNAVEVSVUKQEVWKVEMLAAIJULTWLANAYLDA
FVFIGGVGAQYGDTGRMIFPAGAPASILIWFPLVGFGAAALSRPLSSPKVWRWINVVV
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                                                           translation="MNPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVG"
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dene CDS	gene		gene CDS	gene
	Oy 661 GTGGCAGTTGTGATGCGCATTGGCCATCAAACTGATGTTGATGGTTAG 711	ACTIVICES COTYNEDACTERIUM Glutamicum ATCC 13032 ORGANISM COTYNEDACTERIUM Glutamicum ATCC 13032 ORGANISM COTYNEDACTERIUM Glutamicum ATCC 13032 Bacteria, Actinobacteriua, Actinobacteridae, Actinomycetales, Cotynebacterineae, Corynebacterium. I Addrivor I Asagawa, S. TITLE JOURNAL Unpublished NAKAGAWA, Direct Submission JOURNAL Since Submission JOURNAL Jokyo Bacarch Laboratories, 3-6-6, Asahi-machi, Machida, Tokyo 194-8933, Japan (B-mail:smakagawa@kanagen.com, Tokyo 194-8933, Japan (B-mail:smakagawa@kanagen.com, Tokyo 194-8939, 1031, Fax:81-44-813-1651)	inis Begre SS Co. Ltd. L SS ource 1 ource 2 SS C C C C C C C C C C C C C C C C C C	/ U.Z. T.E.E. S. T. L. S. T. L. L. L. L. L. L. L. L. L. L. L. L. L.

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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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/gene="Cg10953"
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/gene="Cgl0953"
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GLIVDHAVLTKDLRRLVVGLVAFVVLFVVLSFSYRFGSRALRRAVMFBESHLRYBVAD
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AVKTPERASGASRAAVDTAVASGKVAGIGELSIAVNLAAVLLLAGWRVTTGELGPGQ
LIAIVGVAVYLSEPIRLLSNSINASALAHGRAERVANFLNLDESQAQYESSETINDGE
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APTAEPLHILTNVLSELTDRRMPIWIWVRPPVIVGYLIMEVATLYYWAPNARPWKERWL
SLGSFLAIVGILLAGVGLNFYFTLFAAFSSYGAVGSLLAVFIALWYFNICLIIGLKID
VEISRAKQLOAGWPAEDYSLVPFRSIEKVAKKKRQRQORLMDQAAAIREESN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tränglation="WTAWLCSFPSGVQDEYDWANGVVQPQEHLDATLIAADFHGNPEN
SGDRKERLNPQGWKYALNRTVRDVFPDGLLDLAALLTFFSILSIAPAVLLGYSVITIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPSNRTDVCVLDLQLGGIDGIDTATRLMBTTPDLAVLIVTSHARPRQLKRALAAGVLG
FLPKTSTRDEFATALRTVHAGRRYIDPELAAMTISAGESPLTNREEEVLELAGGGLSA
EEIAVAAHLAPGTTRNYLSQAMTKVGAQNRFEAFTRARELGML"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'translation="MKHYWSMYFGAGPLNTPHTKEVWFMDIVSIVNHWFEWSTNNWVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LASDSTEILNLVRDEVNQYVPEDQSHVVNGVIDSIAGSAAAGQVGVAVGVITALWTSS
                                                                                             YTRYSIOMI PVVILGAYFLGIVANAGTIANPSFVWILGFSVILLIVTVIVYEYQPSIAS
HPRRSVQPFFTGLVIAVLGVVSVVLQI PGIAMSDNTRATALI FTITCVFILSIAYI
PWMRYRWYWI IAMSAYLWTSTYTDYLSALWYV IPPIMAGTYBLSVWTVDVMKEVERS
RELEASITURYTERILRPQEIHDTIGQHLAAMSVKSELALALAKRGDRIANELSELGK
LTRYSMSERRUDVSGYRTVALATEI EGANSLIAADAHIHLSVIGTTSQVSPAHRELCAM
LVREATTNILRHSDATDATLILSSTEVRMDNNGVNKDIGRLSGLSALKSRAASBARTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MISISIADDEALIASSLATLLSLEPDLDVRPTAGSGEELIETWA
                                                                                /translation="MNKDFWTAGWTARWFSRGVSLLASPVTAPLNSWRRLPNLAKYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="ABC-type multidrug/protein/lipid transport
                                                                                                                                                                                                                                                                                                                                                                                                       /product="Two-component system, response regulators consisting of a CheY-like receiver domain and a HTH
                                                                                                                                                                                                                                                                                                                        /note="PF00072:Response regulator receiver domain
PP00196:Bacterial regulatory proteins, luxR family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00664:ABC transporter transmembrane region."
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|trans] table=11
|produce="tRNA-processing ribonuclease BN"
|protein_id="BAB98344.1"
|db_xref="GI:21323718"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="Hypothetical protein"
protein id="BAB98343.1"
db_xref="G1:21323717"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="PF00005:ABC transporter
                                                                                                                                                                                                                         IVSREDDQFSVRMLINAPANTPAEKEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system, ATPase component"
/protein_id="BAB98345.1"
/db_xref="GI:21323719"
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/db_xref="G1:21323715"
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/transl_table=11
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trans[_table=11
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/gene="Cg10952"
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/gene="Cg10952"
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transl_table=1
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                                                                                                                                                                                                                                                                                                                                    Gaps
                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                              Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A. Novel polymuclectides
Patent: EP 110870-4 3455 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
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                                                                Corynebacterineae; Corynebacteriaceae; Corynebacterium
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                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                  /organism="Corynebacterium glutamicum"
|mol_type="unassigned DNA"
|db_xref="taxon:1718"
                                                                                                                                                                                                                                                                                                 tch 99.6%; Score 708; DB 6; Le al Similarity 100.0%; Pred. No. 1.5e-168; 708; Conservative 0; Mismatches 0;
                 Corynebacterium glutamicum
Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                    Local Similarity
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BD165656
                                                                                  REFERENCE
                                                                                                  AUTHORS
   KEYWORDS
                                                                                                                                                                                    FEATURES
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Patent: EP 1108790-A 7063 20-JUN-2001;
KYOWA HAKOK KOGYO CO., LTD. (JP)
Location/Qualifiers
                                                                                                                                                                                                                                    Length 349980;
                                                                                                                                                                                                                                     / Match
Local Similarity 100.0%; Score 711; DB 6; Length 3.
Local Similarity 100.0%; Pred. No. 5.9e-169;
les 711; Conservative 0; Mismatches 0; Indels
                                                                                                  1. .349980
/organism="Corynebacterium glutamicum"
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                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:1718"
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(b)	15-DEC-2000 JP 2000405096 SATOSHI NAKAGNA, HIROSHI MIZOGUCHI, SEIKO AN KEIKO OCHIAL, HARUHIKO YOKOI, NAOKO TATEISHI, AKIHIRO SENOO OZAKI CIZNIS/09, CIZNIS/09, COTKL4/34, COTKI6/12, COTCINI/15, CIZNI/15, CIZNI/19, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZNIS/00, CIZN	FT (Organism="Corynebacterium glutamicum". FEATURES 1708 Source 1708 Anol_type="genomic DNA" Ad_xref="taxon:32644" ORIGIN Query Match 99.6%; Score 708; DB 6; Length 708; Best Local Similarity 100.0%; Pred. No. 1.5e-168; Matches 708; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AGTCTTTTACTGTCC	121 GTTCTTCTGGTGTTTAATTCTGACGTCTTTTGTTCATCGCCGCACCTTGGGCGTT 180	241 TACCTGTTATGGTTTGCCGTCATGGCAGCGAAAGACGCCATGACAAACAA

ATGGTGATCATGGAAATCTTCATTACAGGTCTGCTTTTGGGGGCCAGTCTTTTACTGTCC 60	Qy 181 GATCTTTTGTCCAATGCGGCGCCGATCGTGCTGGATGTTATGCGTGGGGTGCGGTGCTC 240 bb 958 GGCTGATCTCCGACCCCCGATCATTCTCGACATCCTGCGTGGGTGCGGTGCGGTCGCTGCCTGC	301 CCACACATATTGAAGAAACAACCAACCGTGCCCGATGACGCCTTTGGGCGGTTCG	1183 GTCTGGGTCAGGCCCATGCCCATTGTGCTGACCTGGCCTAATCCCAATGCCTAC 481 TTGGACGCGTTTGTGTTTATCGGCGCGCGCGCAATACGGCGACCACCGGACGTGG [Oy S41 ATTTTCGCCGCTGGCGCGCTCGCGCGCAACCTGATCTGGTTCGGCTGGGGGGGTTGGCCGCGCGCG	1423 SULT 12 OB3133 AB FUNTION CO FINITION TO CO CESSION AB RSION AB	S CCE CCE CCE CCE CCE CCE CCE CCE CCE CC
Oy 181 GATCTTTTGTCCAATGCCGCGGTCGTCTCGATATTATGCGCTGGGGTGCCTCGT 240 Db 181 GATCTTTTGTCCAATGCCGCGGTCGTCGTTTATGCGCTGGGGTGCTCGCT 240 Oy 241 TACCTGTTATGCTTTTGCCGTCATGGCGAAAGACGCCATGACAAACAA	Qy 360 GGGGGTGGCCACTGACCACGCGCGGGTGGAGGGTGAGCGTCGATAAGCAGG 419 Db 361 GGTTGGCCACTGACGCGCAACCGGGTGCGGGTGAGGTGA	QY 480 TTTGGACGCGTTTGTGTTTATCGGCGCGCGCAATACGGCGACGCGCGCACGCGG 539 Db 481 TTTGGACGCTTTTATCGGCGGCGCGCGCGCAATACGGCGACCCGGACGGTG 540 Db 540 GATTTTCGCCGCTTGGCGGTTCGCGCAACCTGATCCGCTGGTGGGGTTTCGG 599 Db 541 GATTTTCGCCGCTTGCCGGTTGCGGGACAGCTGATCCGGTGGTGGGGTTTCGG 599 Db 541 GATTTTCGCCGCTTGCCGGCAAGCTTGTTCGGGAATCAGGTTCCGGTGGGGTTTCCG QY 600 GGCAGCAATTGCCGCCTGTCCCAGCCCAAGGTTGCCGCTGGTGGGTTTCGG QY 600 GGCAGCAATTGCCGCCCGTGCCCCAAGGTTGCCCCAAGGTTGAACGTCGT	660	RESULT 11 ES4483 LOCUS LOCUS DEFINITION Heat-resistant lysine biosynthesis enzyme gene of thermophilic COTYNEform bacterium. ACCESSION E54483. G1:22553540 KEYMORDS JP 2001120270-A/7. SOURCE COTYNEFORM the part 27-AUG-2002 ACCESSION B54483 SOURCE COTYNEBACTERIUM thermoaminogenes	NIS! NCE DORS E NAL	H H H H H H H H H H H H H H H H H H H

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Evaluation, Shibuya-ku, Tokyo, 151-0066 Japan.
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                                                                                    1446 chddandcchhcdrchtandgengengengeccaagacagagagacagargagaga
                                                481 TTGGACGCGTTTGTGTTTATCGGCGCGCGCGCGCGCAATACGGCGACCCGGACGGTGG
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Corynebacterium efficiens YS-314 DNA, complete genome, section
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Sugimoto,S., Matsui,K., Yamagishi,A., Kikuchi,H., Ikeo,K. and
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Director-General of Biotechnology Center.
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llarity 67.7%; Pred. No. 1.5e-69;
Conservative 0; Mismatches 214;
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                                   Fax:81-44-222-0129)
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/trānslation="krtycykkaligivavigsgilvaggsydprrebeherovaedk
Enlytavdpdylghnviselyktvighrgreavirhedniladpedplnegtsdlvig
Ctgalievnpvlagelestlaavergeetinsgebrryppaligselseridadp
Straklestynsvipavivpiyrnptesradreilnwasgaittselgeliebakeigr
Relvkefvaskgg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (translation="wsmoatgsggnrraelglkkrpegwpvgsfgtyeeaqravdmls
Dnefpvaeltivgvdlmevetvtgrltmgrvlaggaasgamlglffglvmglvsnlmf
SSLLtglvmgvvfgvvlaavpywasrgkrdftsatqivagrydilcrpdrareardmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /trānslation="MRTILIGVLLFVAACVQCAIGFGLGMLAAPITALMRPDLLFGLI
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ILGTLISLVGWSPGHGRRNSFLAGASGGFLGTTTAIGGPPLALIMRSMSPERVRGTLS
VCFVIGSAISTALINGAGALGWMHLQAALVYAPAVIAGYFLSGVVNKHLNFRLIFIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tränglation="MGRGDGFFAERFPAADPRCGRKTTIMGROTKGALAAAAALLIV
GGGGGTENSWINEVTGRODALAAAAAAAGAAAGKWTINGQDVUDNNVAAVKVVPGDTLV
TTQQISYETGGDNIGATLTILTPGSITGATADAADAALATELNDTTTIDLGELPTSITG
SGNTYTFEGGVRGSGVSALSIKQAA"
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PYLYVSCDALTMKVREGGRVVKTSVLLATGVNABGYRELLGMQVATAESYASWTGFFR
DLKARGLABYLVTSDAHLGIQIALGSVLFWASWQRCFHFFSKNLYGWVSKTQWPTLS
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WSNNFTERLABTRRTDVVGIFPNRDAVYRLVGAVLAEQHDDWIQQKRYWSLTSLEQ
TRAMMTANIIDSDDITSEIIRKDVA"
complement (11439. .15143)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tränslation="maagpysidpttyldbillaqaspdlmremlggfinqilstqadq
vcgadyatvsqdrvntrngyrhrdfdtrvgtidvavpxlrtgsffpdmllbrrtrarr
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QELSEDRQAELIETLDIRRAADVLBEMDPDDAADLLGELPEDKAGVLLELMDPEESAP
                                                                                                                                                              VRRIMGFNPDTVCALMTPEPLIMDPSTTVAEALAMARNPDLPTSLASLVFVVRPPTAT
PTGKYLGCVHLQKLLREPPSSLVGGILDPDLPPLYANDSQETAARFFATYNLVCGPVL
                                     GLVVELVNNKRRIFLPMLRIAAIEPKEVNLISGSVSLRSFKARTGELQVIGDIIGTK
                                                                    VHTDDPELEQLHGRAVEIADVELEQTRTRDWVISRVALIGERPKFGRRPTLYIAPWSH
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/note="CE1189, similar to AF024666-23 AAG03374.1 percent
identity: 84 in 408 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="CE1187, similar to AE007262-3|AAK65408.1| percent flentity: 32 in 235 aa" /codon Btart=1 /trans1_table=11
                                                                                                                                                                                                                                                                     5264. .5782
'note="CE1185, similar to AE007003-6|AAK45530.1| percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="conserved hypothetical protein"
/protein.id="BAC17997.1"
/db_xref="G1:23493026"
                                                                                                                                                                                                                                                                                                                                                                                                                        product="conserved hypothetical protein"
/protein_id="BAC17995.1"
/db_xref="GI:23493024"
                                                                                                                                                                                                                               DENGHLIGAVAVDDLLDHMLPEDWRDAGIRPGVKEETLG
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/product="hypothetical protein"
/protein id="BAC17998.1"
/db_xref="GI:23493027"
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/protein_id="BAC17996.1"
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/protein_id="BAC17999.1"
/db_xref="G1:23493028"
                                                                                                                                                                                                                                                                                                                               dentity: 60 in 155 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'db xref="GI:23493025"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WIISLIGSGMVITQAAGIF"
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trans table=11
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/transl_table=11
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'note="CE1188"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5805. .6500
/note="CE1186"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARNMGELGHPRQ"
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Lfwgtifviiwiminiggfawnwdpypfiliniafstgaayaapliilagnrqedrdk
Stiladrrraeetyadteflyrelagyrlaygewytrdyirhelddlkgflerleakl
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'translation="MTTGIILGTVGPGDAGLAKLGSDIPRGVGIEHRPRKPPVALQYR
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LVHCAECRQEIARQRDTVDFVRTECRNDNVTAPSDLKAKLMSLANECAPGPGAEDAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNAKQNLDTDFGEEFDEIRKPMAQIAQIRSMSPKTAITRALFDGDDSFLDSFDPKKIM
ADDTAGQAHRQQVAKTGTTPEHAEVVERPADRIDPTQSPNTPGKNNDGGRPPAGGGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGSDARPHQVDDMIMPPQAHGVKMISIAHFVEGNAPVVWRGPMLHRAIQQFLSDVFWG
DLDLILLDDFPGTGDIAILTAQLENAELLITYTPQAAAANVARRAGSISLGTNQKVA
QVIBNMSAWWPDGSTWEVGGSGGGEKIAQRLSMLTGEDVPVLGSVPLDPSLRVGGDV
GNPIAISEPYSPTTAAINAIADILAKRRVSIVGKTLGLGVK"
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DLEEVYTRDYTAXELPYDLEQIFGTLASI PYDVGLASKKAAEHLDAGALLMTALRRNG
POPTRVSKLL RAKRRKLFPI FDSAI KRQLNTNSVGFYENFHTVLRAEDKALSRHLKGI
RTEAADQSGNSALADLSTIRVFDVVVWMADHKRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MFSNVGWGEILLLFIVGLIVIGPERLPRLMEDLKAAIVAARTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MMSQVTESAVRSALSRVEDPEIGKPITELGMVKSVAIDGSDVQV/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVYLTIAACPMKTTIVSNTEAAIKDIEGVGDVQVTTDVMSDEQRRELRVSLRGNTADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VI PFAQPGSTTRVYAVASGKGGVGKSSMTVNLATALAAKGLSVGILDADIYGHSVPGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="CE1181, similar to AL390975-15|CAC01353.1| percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1829. .5124)
/note="CEI184, similar to AE007003-4 | AAK45528.1 | percent
identity: 52 in 417 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            774. .1271
/note="CE1180, similar to AJ292256-1|CAC21724.1| percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (3282. .3836)
/note="CE1183, similar to AE007003-3|AAK45527.1| percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative ATP-binding protein Mrp"/
/protein_id="BAC17991.1"
/db_xref="GI:23493020"
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/protein.id="BAC17993.1"
/db_xref="G1:23493022"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
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/protein_id="BAC17992.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      QRPESFVAKVESVVRAVRRTQGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identity: 26 in 155 aa" /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (1353. .2480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identity: 63 in 370 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (2513. .3271)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="CE1182"
/codon start=1
/trans1_table=11
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/transl_table=11
                                                                                                                                         365. .742
/note="CE1179"
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GKSTLLKSFARILQPHTGQVYTGDNPLDSLHTKYTAQRIALLEQTALAPADITVEBLV
GRGRPTYLLKQWSTYDAQAVDSALLATGTAQLEHRRYTELSGGGRQRVWLAMVLAQ
RYPVYLLDEQWSTYDAQAVGGLLELARALRQQLGRTYTVHDLQQAVRYADHLIVMK
GGAVYABGAPSSIMTPQLISBVFDINVDVHTIDDHVVIVPKTMPQQPDVSVLENLQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAE49578.1"
/db_xref="G1:88199913"
/translation="MLIDMILAFSVAPTETRNNKARMADVVAEAIRVVRESGLPNETN
AMPTLIEGEMOEVMAVXKATDAVLAVSPPAASIVIKADIRPGYTGGLQQKVASVERVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus tag="DIP1058"
/note="HMMPfam hit to PF01910, Protein of unknown function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="HMWSmart hit to SM00382, ATPases associated with a variety of cellular activities" complement (567. .1130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="DIP1058"
/note="finitar to Mycobacterium tuberculosis hypothetical
11.0 kba protein Rv1689 or WT1949 or WTCY180.20c
8W:Y198 MYCTU (007734) [102 aa) fasta scores: E():
5.8e-16 56.43% id in 101 aa, and to Aquifex aeolicus
hypothetical 17.9 kba protein AQ_2067 TR:067847
(EMEL:AE000771) [157 aa) fasta scores: E(): 4.7e-08,
40.19% id in 102 aa"
                                                                                                                                                                                                                                                                                                         Submitted (03-0CT-2003) Cerdeno-Tarraga A.M., submitted on behalf of the Pathogen Sequencing Unit, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail:
Rabbinowitsch, E., Rutherford, K., Thomson, N.R., Unwin, L., Whitehead, S. and Barrell B.G. Parkhill, J. The complete genome sequence and analysis of Corynebacterium diphtheriae NCTC13129
Nucleic Acids Res. 31 (22), 6516-6523 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(405, .4762)
/note="Putative iron uptake system. Low GC content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Putative iron-siderophore uptake system
/product="Putative iron-siderophore uptake system
/protein id="CAE49580.1"
/db_xref="GI:38199914"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trans<u>T</u>table=11
/product="Conserved hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Corynebacterium diphtheriae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1e-41, 49.61% id in 262 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="NCTC13129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (564. .1133)
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/locus_tag="DIP1059"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .349535
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                                                                                                                                                                                                                                                Cerdeno-Tarraga, A.M.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                        61 ATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GITCTICTCGTGTGTTTAATTTCTGACGTCTTTTTGTTCATCGCCGGCACCTTGGGCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GITTGGGTAAAGCCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGGAATGCGTAT
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                                                                                                                                                                                      Gaps
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                                                                                                               Length 308650;
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                                                                                                                                                                                   Indels
                                                                                                                  Score 317.6; DB 1;
Pred. No. 2.9e-69;
0; Mismatches 214;
                                                  complement (11439. .15143)
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Corynebacterium diphtheriae
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BXZ48357.1 GI:38199912
                                                                                                                  Ouery Match
Best Local Similarity 67.7%;
Matches 481; Conservative
                 /gene="odhA'
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37261 TCGGGCCACAAAATGCCTTGATTATTCGTCAAGGCATTAAACGCGAAGGTCTAATCCCCA 37202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77081 ACTTGCTCTATTTCGGATTCACTTGTTTTAAAGAAGCATTTAAACGTCACGGCCAAGCGC 37022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37021 receacric - - checannecances accoración acardes reconstructudos 36965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus tag="DIP1061"
/noche="Signal peptide predicted for DIP1061 by SignalP 2.0
/noche="Signal peptide probability 1.000) with cleavage site
probability 0.663 between residues 34 and 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                       /translation="MLRQPRVRLPLPLVITFLVIILLCTIIMSLGVGARNITSPDILA
                                                                                                                                                                                                                                                              ALRHYGDPTNSHIIWGRRIPRTLIAIAAGASISLAGVLIQALTRNPLADTGVFGINAG
AAFTIVIGIALAGSLSHISIFALALLGAILAGACVYALSMNSCKGSDPLRLVLAGVAL
                                                                                                                                                                                                                                                                                                                                       SAILTGIGDGLSLYNPQAFDRLKSWMYGNIDAGSYQPAAVAGVGLILGILVTATCMRQ
                                                                                                                                                                                                                                                                                                                                                                                   INALSLGDELAITMGASIAKTRLFTFIAIVVLAASATAAAGVITFLGLMVPHIARMIV
GPNLLRLVATASLIGPIIVLSADILGRIIVPGEFPAGVVVAFIGAPFLIAYAQTKRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signal-periode site accompliance and accomplement (2199. 2225)
/locus tag="DlateErobom hit to PD001557, PD001557"
/note="Riament (2205. 3095)
/locus tag="DlateErobom hit to PP01032, FecCD transport family"
/note="HAMPFam hit to PP01032, FecCD transport family"
order(complement (3096. 3161), complement (2934. 2990),
complement (260. 2735), complement (2766. 2831),
complement (2094. 2459) complement (2244. 2609),
complement (2211. 2276))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 CGGTGGCCACTGACACGCGCAACCGGGTGCGGGTGGAGGTGAGCGTCGATAAGCAGCGGG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 TTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATT 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="DIP1062"
hote="Similar to Escherichia coli iron(III)
dicitrate-binding periplasmic protein precursor FecB or
B4290 SWF.FECB ECOLI (P15028) (300 aa) fasta scores: E():
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37141 gegeaitagregategadeeeeereeeragractagractgaaatgeereggrefer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 TCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 INCITCICGIGIGITITIANITICIGACGICITITIGITICATCGCCGGCACCITGGGCGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="9 probable transmembrane helices predicted for DIP1061 by TMHMM2.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 ATCTTTTGTCCAATGCCGCCCGATCGTCGTCGATATTATGCGCTGGGGTGGCATCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 ACCIGITATGGTTTTGCCGTCATGGCAGCGAAAGACGCCATGACAACAAGGTGGAAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TGGTGATCATGGAAATCTTCATTACAGGTCTGCTTTTGGGGGCCAGTCTTTTACTGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 CACAGAICATIGAAGAAACAGAACCAACGIGCCCGAIGACACGCCTITGGGCGGTICGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Gaps
            (transl table=11
product="Putative iron-siderophore uptake system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 349535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
19.2%; Score 136.6; DB 1; Length 34
Best Local Similarity 52.4%; Pred. No. 2.2e-23;
Matches 354; Conservative 0; Mismatches 309; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36964 GAGTGATCACTAAAACACGCACAAAAGCTCAGCCCAAGTCAGC----
                                                                                          transmembrane component"
/protein_id="CAE49584.1"
/db_xref="GI:38199916"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (3090. .3191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 locus tag="DIP1061"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                locus_tag="DIP1062"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .4282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 엄
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/locus tag="DIP1060"

/locus tag="DIP1060"

/note="Signal peptide predicted for DIP1060 by SignalP 2.0

HWM (Signal peptide probability 0.966) with cleavage site probability 0.180 between residues 25 and 26;

signal-peptide site"

complement (1244...216)

/locus tag="DIP1060"

/note="HWMPfam hit to PF01032, FecCD transport family"

order (complement(2105...2161), complement(1879...2044),

complement (148...1939), complement (1607...1657),

complement (147...1303),

/locus tag="DIP1060"

/note="9 probable transmembrane helices predicted for DIP1060 by TMHPM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Similar to Streptomyces coelicolor putative iron-tion-siderophore uptake system transmembrane component esci51.27C TR:09S213 (EMBL:AL109848) (348 aa) fasta scores: E(): 8e-36, 36.53% id in 323 aa, and to Escherichia coliferric enterobactin transport system permease protein fepD cor BOSO SW:FEDD ECOLI (P23876) (334 aa) fasta scores: E(): 5.2e-40, 40.37% id in 322 aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iron-siderophore uptake system transmembrane component sci51.26C TR:098214 (EWBL:AL109848) (375 aa) fasta scores: E(): 5e-40, 40.74% id in 324 aa. and to Escherichia coli ferric enterobactin transport system permease protein fepg feep or B0589 SN:FEPG ECOLI (P2877) (330 aa) fasta scores: E(): 1.8e-45, 74.09% id in 322 aa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transI_table=11
/product="Putative iron-siderophore uptake system
transmembrane component"
/protain_id="CAE49582.1"
/protain_id="CAE49582.1"
/db xref="0f1:38199915"
/translation="MRALVILSSLLLVTAAAYSLVIPGAGLSTWOLLTSETPLAHTVVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QWRLPRVVTGILVGAALAIAGSLFQSLTRNPLGSPDIIGFSTGÄYTGVIAAFLLGWSG
FGATITGAALGGLASVVYTALSVERTRIDGETIILVGGLSAAMLSANRWLITRGELD
TALSAASWGGSLNGIRWTIAIPACVLAILITTTIPLRFLDVLSLGDDLAVGHGLE
LQLTKLLLVGGVFLVAATTAVAGPIAFVALASPHIARALISSARTPLVETSVIGALL
                                                                                                                                                                        /note="ProfileScan hit to PS50100, 2nd half motif for nucleotide binding, associated with P-loop." complement(751,77)
/locus tag="DIP1059" / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note="ScanRegExp hit to PS00211, ABC transporters family / note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + Note + 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="ScanRegExp hit to PS00017, ATP/GTP-binding site motif A (P-loop)." complement(1223. .2182)
                                                                                                                                                                                                                                                                                                                                                                                                                         complement (1047. .1124)
/locus tage_npInJoS9"
/locus fage_npInJoS9"
/note="ProfileScan hit to PS50101, P-loop nucleotide binding motif (does not find all)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Similar to Streptomyces coelicolor putative
/locus_tag="DIPNO59"
/note="HMMPFam hit to PF00005, ABC transporter"
complement(579. .797)
/locus_tag="DIPN059"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1250. .1564)
/locus_tag="DIPI060"
/note="BlastProDom hit to PD001557, PD001557"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIVADLIGQRLFYPTQLPVGLVTVTIGGMYLLWLIARGSKENS"
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/locus_tag="DIP1061"
complement (2184. .3191)
/locus_tag="DIP1061"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (1223. .2182)
/locus_tag="DIP1060"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (1086. .1109)
/locus_tag="DIP1059"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="DIP1060"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                       signature."
                                                                                                   misc feature
                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                  misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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DPDREPPFFCKPADAVRYVADGTTGGFVYPTETRDCHYEIBLVVALGTGGRDIAVES
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Gene name confidence : hypothetical
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S Boucher, C.A.

Boucher, C.A.

Direct Submission

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Christian.Boucher@toulouse.inra.fr
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                                                                                                                                                                                                   36853 TAGACGTTCTTGTCATGTTGGGAGGAATCGCCAACCAACGGTCCCGACGGGCGCGCTGGG 36794
36793 icticiscicticsciariangisciscas as 38734
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Genome sequence of the plant pathogen Ralstonia solanacearum Nature 415 (6871), 497-502 (2002)
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                                                                                                                                                                                                                                                                                 542 ITTITCGCCGCTGGCGCGTICGCGGCAAGCCTGAICTGGTTCCCGCTGGTGGGTTTCGGCG
                                                                                                                      TGGACGCGTTTGTGTTTTATCGGCGCGCGCGCGCAATACGGCGACACCGGACGGTGGA
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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Ralstonia solanacearum GMI1000 chromosome, complete sequence;
segment 3/19.
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Location/Qualifiers
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AL646059.1 GI:17427391
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| complement (3924 . 3910)
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KSYTPAQVQQVAKTYFTEDNLVVATLLPQPI DPNKPARKPVPGMREEGGLR"
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/note="product confidence : putative
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predicted by FrameD"
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(c) 1993 - 2004 Compugen Ltd.
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The present invention relates to DNA encoding variants of protein with loop region and six hydrophobic helixes which facilitates excretion of L-lyshine and/or L-arginine to outside of cell of a methanol assimilating bacterium when introduced into the bacterium. The method is used for encoding a protein which facilitates excretion of L-lyshine, L-arginine or
                                Aca38373 Prokaryot
Aca40558 Prokaryot
Continuation (21 o
Continuation (21 o
                                                                                                              Adb68842 Minority
Adb68842 Minority
Acf39391 Mycobacte
Continuation (8 of
Continuation (8 of
                                                                                                                                                                                                                            Prokaryot
M. echino
Prokaryot
                  C. glutam
Prokaryot
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Prokaryot
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Abx47227 Bovine ES
                                                                                                                                                                                                                                                                                Pseudomon
                                                                                                  Prokaryot
                                                                                                                                                                                                                                                                                                 Prokaryot
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                                                                                                                                                                                                                                                                                            Aca43878 B
Aca38495 B
Aca40313 B
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                  Aas96096
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ACA27310
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/product= "lysE protein"
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ACA38495
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                  96096SAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACC80941 standard; DNA; 711
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nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
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                                               Corynebacterium glutamicum.
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   both of these L-amino acids to outside of a cell of a methanol assimilating bacterium when DNA of the method is introduced into the absterium. The present sequence represents a lysE protein from Brevibacterium lactofermentum encoding sequence. (Updated on 27-OCT-2003 to standardise OS field)
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Best Local Similarity 100."
Matches 711, Conservative
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                                                                                                                                                                                             AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79534 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleosides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 ATGGTGATCATGGAAATCTTCATTACAGGTCTGCTTTTTGGGGGCCCAGTCTTTTACTGCTC 151
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                                                                              metabolic pathway
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                                                                              Nucleic acids from Corynebacterium glutamicum encoding metabolic pathw
proteins, useful for producing fine chemicals in microorganisms,
including organic acids, nonproteinogenic amino acids, and purine and
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Haberhauer G;
                                                                                                                                                                                                                                                                                                                                                               'Match 100.0%; Score 711; DB 4; Length 822; Local Similarity 100.0%; Pred. No. 4.2e-206; es 711; Conservative 0; Mismatches 0; Indels
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Zelder
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Schroeder
Kroeger B,
                               WPI; 2001-137957/14.
                                                P-PSDB; AAB79660.
                                                                                                                              pyrimidine bases.
Pompejus M,
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The present invention relates to the isolation of novel Corynebacterium glutamicum genes encoding metabolic pathway (MP) proteins (AMU71863-AAU71922). The metabolic pathway proteins of the invention include enzymes involved in the lyshine and methionine biosynthetic pathways. The polywucleotide sequences of the invention can be used for the large-scale production and/or modulation of expression of fine chemicals such a lyshine and methionine. The sequences of the invention may be used to identify C. glutamicum and related organisms e.g. C. diptheriation in a subject to detect diptheria. AASS9673-AASS96132 represent C. glutamicum apenes encoding the novel metabolic pathway proteins of the invention
                                                                                                                                                                                                                                                                                           Metabolic pathway protein; MP; lysine biosynthesis pathway;
methionine biosynthesis pathway; large-scale production of fine chemical;
Corynebacterium diphtheriae; diphtheria; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGGAAGGACTCATTGCG
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                                                                                                                                                                                                                           C. glutamicum gene #23 encoding metabolic pathway protein
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100.0%; Pred. No. 4.2e-206;
tive 0; Mismatches 0;
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В.
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23-JUN-2000; 2000US-00606740.
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AAS96098 standard; DNA; 822
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I, Hwang B;
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                                                                                                                               GTTTGGGTAAAGCCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGGAATGCGTAT 480
                                                                                                                                                                         TIGGACGCGTITIGIGITITATCGGCGCGTCGCCGCGAATACGGCGACACCGGACGGTGG 540
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                                                                                                                                                                                       541 ATTITCGCCGCTGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGC
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rececerace
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding LysG, LysE and ORF3 from Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                      GTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATGGGTTAG 711
                                           CCACAGATCATTGAAGAAACAGAACCAACCGTGCCCGATGACACGCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This DNA, isolated from Corynebacterium glutamicum, contains the LysG, LysE and ORF3 genes. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene. NB. This sequence has been created from the information given in table 2 of the
                      improving export carrier activity or corresponding gene expression, also new export and regulatory genes from Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 GCGGTGGCCACTGACACGCGCAACCGGGTGCGGGTGGAGGTGAGCGTCGATAAGCAGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 2374;
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Local Similarity 100.0%; Pred. No. 6.9e-206;
ies 711; Conservative 0; Mismatches 0;
P-PSDB; AAW37714, AAW37715, AAW37716.
                                                                                                         Claim 23 and 26; Page; 16pp; German.
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                                                                                               1196 GATCTTTTGTCCAATGCCGCGCGATCGTGCCTCGAATTTATGCGCTGGGGTGCCATCGCT
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Senoh A, Ikeda M, Ozaki A;
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07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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Tateishi N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a method for producing L-arginine in a microorganism (e.g. coryneform bacteria) that has L-arginine producing ability and has been modified for enhanced expression of the lysE gene. The microorganism is also modified so that an arginine repressor (argR) does not function normally. The method of the invention is useful for the enhanced production of L-arginine which is useful in liver function promoting agents, amino acid influsion and comprehensive amino acid pharmaceuticals. The present sequence represents a DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1016 Argercarcargaaarcrrcarracagercrecrrrregegeccagrcrrracrercc 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A microorganism comprising enhanced expression of the lysE gene is useful for enhanced production of L-arginine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-arginine production, coryneform bacteria, lyBE, arginine repressor, argR; liver function promoting agent, amino acid infusion, amino acid pharmaceutical; LysG, ds.
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1676 GTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATGGGTTAG 1726
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                                                                                                                                                                                                                                                                                                                                                                                     DNA fragment containing C. glutamicum LysG and LysE genes.
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1025. .1726
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Best Local Similarity
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AAH68420 standard; DNA; 708

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28533 GTTTGGGTAAAGCCCATGTTGTTGTTGTGTGTGACCTGGTTGAACCCGAATGCGTAT 128474
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                                                                                     The present inventions provided a number of the seequence from the CoryneCorm bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of corpneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, corpneform bacteria are useful for producing amino acids, nucleic acids, vitamins, asccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 349980 BP; 80727 A; 91049 C; 97618 G; 80586 T; 0 U; 0 Other;
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Disclosure; SEQ ID NO 7063; 246pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 100.0%; Score 711; DB 5; L Local Similarity 100.0%; Pred. No. 7.2e-205; les 711; Conservative 0; Mismatches 0:
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, coryneform bacteria are useful for producing amino particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the Buropean Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AICGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGGGCGAAGGACTCATTGCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Yokoi
                                                                                                                                  Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       H, Ando S, Hayashi M, Ochiai K,
Ikeda M, Ozaki A;
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                                                                                                C glutamicum coding sequence fragment SEQ ID NO: 3455
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2000JP-00159162.
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                                                                                                                                                        organic acid synthesis; ds.
                                                                                                                                                                                          Corynebacterium glutamicum.
                                                                   (first entry)
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Matches 708; Conservative
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Tateishi N,
                                                                   26-SEP-2001
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The present invention relates to DNA encoding variants of protein with loop region and six hydrophobic helixes which facilitates excretion of L-lysine and/or L-arginine to outside of cell of a methanol assimilating bacterium when introduced into the bacterium. The method is used for both of these L-amino acids to outside of a cell of a methanol assimilating bacterium when DNA of the method is introduced into the bacterium. The present sequence represents a lysE24 protein from bacterium lactofermentum encoding sequence. (Updated on 27-OCT-2003 to standardise OS field)
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                                                                                                                                                                                       Length 712;
                                                                                                                                                          Sequence 712 BP; 133 A; 173 C; 224 G; 182 T; 0 U; 0 Other;
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                     Score 696.8; DB 8;
Pred. No. 8.3e-202;
0; Mismatches 2;
                                                                                                                                                                                       Query Match 98.0%;
Best Local Similarity 99.6%;
Matches 709; Conservative C
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                                                                                                                            GTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTTGACCTGGTTGAACCCGAATGCGTAT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel DNA encoding variant of LysE protein from a coryneform bacterium, when introduced into methanol assimilating bacterium, facilitates excretion of L-lysine and/or L-arginine to outside of a cell.
                                                                   ATTITCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGC
                                                    CCACAGATCATTGAAGAAACAGAACCAACGTGCCCGATGACACGCCTTTGGGCGGTTCG
                                                                                                         GCGGTGGCCACTGACACGCGCAACCGGGTGCGGGTGGAGGTGAGCGTCGATAAGCAGCGG
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11-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACC80942;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In this case, an increase in arginine, glutamic acid and lygine is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli
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541 ATTTTOGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGC
                                     GCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCCAAGGTGTGGCGCTGGATCAACGTCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B. coli; yggA gene; amino acid production; excretion protein gene;
amino acid excretion protein; ds.
                                                                                                                                                                                                                                                             1423 GTGGCCGTGGTGCTCCCGGATTGGCCGTGAAGCTGATCCTGATGGGTTA 1472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aleshin VV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakanishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/product= "YggA"
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99RU-00104431.
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                                                                                                                                                                                                                                                                                                                                                                                                                             AAA52691 standard; DNA; 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli yggA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a gene from a high temperature-resistant coryneform microbe that encodes a heat-resistant lysin biosynthetic coryne. The enzyme has aspartete-semialdehyde dehydrogenase activity and can be used for growing amino acid-producing microbes. The present sequence encodes an enzyme of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match Local Similarity 67.7%; Pred. No. 4.8e-86; Length 68 481; Conservative 0; Mismatches 214; Indels
                                                                           Heat-resistant; lysin biosynthesis; enzyme; coryneform;

    C. thermoaminogenes lysin biosynthetic enzyme lysE DNA.

                                                                                                        aspartate-semialdehyde dehydrogenase; lysE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 temperature-resistant coryneform microbe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Page 22-24; 27pp; Japanese.
                                                                                                                                                             Corynebacterium thermoaminogenes
                                                                                                                                                                                                                                                                                                                                     99JP-00311148
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                                Sequence 15239 BP; 2878 A; 4791 C; 4729 G; 2841 T; 0 U; 0 Other;
                                                                                                                                                                                            3;
                                                                                                      Ouery Match 8.0%; Score 57; DB 2; Length 15239; Best Local Similarity 53.1%; Pred. No. 4e-06; Matches 145; Conservative 0; Mismatches 125; Indels
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BCGdelta2. A specific genetic deletion of this region results in an
avirulence phenotype of the mycobacterium. 2 other deletion regions (see
AAT3355 and AAT3357) have also been detected. Identification involved
screening a BCG cosmid library with a radiolabeled probe obtained
screening DBCG cosmid library with a radiolabeled probe obtained
screening DBCG cosmid library with a radiolabeled probe obtained
following DNA subtraction between virulent Mycobacterium tuberculosis
H37Rv and avirulent BCG. The deletions provide useful markers for the
identification of an avirulence requires the detection of the presence or
absence of the deletion; the deletions are detected either by detecting
the presence or absence of deletion junctions (see AAT33538-46), or by
detecting the presence or absence of the sequences contained within the
deletion. Deletion polypeptides are used as components of immunological
assays and in vaccines. (Updated on 16-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                        199 GCGCCGATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCTTACCTGTTATGGTTTGCC 258
                                                                     79 CIGGIGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCGGTTCTTCTCGTGTTTA 138
                                                                                                                                                   73 rirgigaigaarcagggaraaggcercegracercararaarracerracrrigiecr 132
                                                                                                                                                                                                                                 139 ATTICIGACGICITITIGITCALCGCCGCCACCIIGGCCGIIGALCITITGICCAAIGCC 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 TTTGGCGCTTTTAAAACAGCAATGAGCAGTAATATTGA 290
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ID AAT33536 standard; DNA; 15239 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polynucleotide sequence that is highly conserved in both genomes with no
                                                                                                                                                                                                                                                                                                                                    490
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                                                                                                                                                                                                                                                                            0; Mismatches 125; Indels
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                                                                                                                                                                                                                                                                                                                                                           64736 CATTCTTCGCAACTCCAGCTGCTTGGCGCATTCTTGATGCGCTGGTTGCCGTGACGATGA 64795
counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a Mycobacterial cosmid DNA sequence used in the method of the invention
                                                                                                                                                                                                                                                                                      557 CGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGGTTTCGGCGCAGCAGCATTGTCAC 616
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Continuation (6 of 45)
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RESULT 2
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Sequence 4674, Ap
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Sequence 800, App
Sequence 15639, A
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Sequence 17, Appl
Sequence 2, Appli
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Sequence 7643, Ap
Sequence 7841, Ap
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1099, Ap
989, App
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2121, Ap
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7366.769 Million cell updates/sec
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                                                                          March 15, 2004, 13:47:35; Search time 53.5608 Seconds
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           GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-839-878-17

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Listing first 45 summaries
                                                    - nucleic search, using sw model
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GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: 1879-102-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
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Sequence 1455, A
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Sequence 1586, Ap
Sequence 1577, A
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Pred. No. 4.9e-09;
0; Mismatches 117; Indels
US-09-252-991A-1216

US-09-252-991A-1163

US-09-252-991A-14676

US-09-252-991A-14676

US-08-222-991A-15078

US-08-608-004-2

US-08-608-004-2

US-08-402-608-2

US-08-402-608-2

US-09-252-991A-15856

US-09-252-991A-15779

US-09-252-991A-13779

US-09-252-991A-13776

US-09-252-991A-13756

US-09-252-991A-13565

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511 TOTCACGCCCGCTGTCCAGCCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGCAGTTG 670
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500 TCGGCGGCGTCGGCGCGCAATACGGCGACACCGGACGGTGGATTTTCGCCGCTGGCGCT
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APPLICANT: Behr, Marcel
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TITLE OF INVENTION: Molecular Differences Between Species of
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CURRENT APPLICATION NUMBER: 08/09/894,844
CURRENT APPLICATION NUMBER: 09/318,191
PRIOR APPLICATION NUMBER: 60/097,936
PRIOR FILING DATE: 1998-08-25
PRIOR PELLOR DAS: 137
SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 17, Application US/08390878
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                           APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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GENERAL MAC J. Rubenfield et al.

TITLE OF INVENTION: NUCLECC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAFEUTICS

FILE REFERENCE: 107196.136

CURRENT REPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

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PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 7841
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Pred. No. 5.5e-09;
0; Mismatches 117; Indels
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Pred. No. 5.3e-09;
0; Mismatches 117; Indels
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 54.6%;
Matches 148; Conservative (
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TITLE OP INVENTION: TUBERCULOSIS
FILE REPERBERGE. 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
SOFTWARE: PATENTIN NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                                    TYPE: DNA ORGANISM: Mycobacterium tuberculosis
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Matches 145; Conservative
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Patent No. 6294332
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRESK, Claire M.
APPLICANT: PRASK, Claire M.
APPLICANT: WENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Gaps
                     APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SIGURENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 15239;
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8.0%; Score 57; DB 1; Length 152
Best Local Similarity 53.1%; Pred. No. 6.6e-07;
Matches 145; Conservative 0; Mismatches 125; Indels
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/390,878
FILIAG DATE: 17-FEB-1995
CLASSIFICATION WIMBER: US/08/390,878
FILIAG DATE: 17-FEB-1995
ATTORNEY/AGENT INPORMATION:
RAGISTRATION NUMBER: 15.371A-17
TELECOMMUNICATION INPORMATION:
TELEFRAX: 415/543/5043
INPORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15239 base pairs
TYPE: MIGLER ocid
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CITY: San Francisco
STATE: California
COUNTRY: USA
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            GENERAL INFORMATION:
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US-09-103-840A-2
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OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: YENSER, Claire M.
APPLICANT: YENTER, JOHN C.
TITLE OF INVENTION: DAS EQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT PAPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2.1
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Pred. No. 1.1e-05;
0; Mismatches 125; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                  Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.0%; Score 57; DB 3; Length 440.
Best Local Similarity 53.1%; Pred. No. 1.1e-05;
Matches 145; Conservative 0; Mismatches 125; Indels
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Sequence 800, Application US/09543681A

Sequence 800, Application US/09543681A

Patent No. 666770

GENERAL INFORMATION:
APPLICANT: GARY BRETION:
TITLE OF INVENTION: ULCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: ULCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709, 1002-001
FILE REFERENCE: 2709, 1002-001
FILE REFERENCE: 2000-04-05
FILE REFERENCE: 2000-04-05
PRIOR PAPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53.8; DB 4; Pred. No. 1.7e-06; 0; Mismatches 107;
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7571
LENGTH: 1176
                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.6%;
Best Local Similarity 54.3%;
Matches 134; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.0%
Query Match
Best Local Similarity 46.7%
Matches 136, Conservative
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US-09-543-681A-800
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                                                                                                                                                                                                                                                                                                                TYPE: DNA
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FALCENT NO. 2017/20

APPLICANT: MATC J. RUDENTION: ALBENDATION ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Gary Breton et, al

APPLICANT: Gary Breton et, al

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1209-121

PRIOR PPLIATION NUMBER: US 60/117,747

PRIOR PPLIATION TOWER: 1999-101-29

NUMBER OF SEQ ID NOS: 14342
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Pred. No. 1.8e-07;
0; Mismatches 139;
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US-00-22-991A-7571/c
Sequence 7571, Application US/09252991A
; Patent No. 6551795
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Patent No. 6610836
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Best Local Similarity 50.2%;
Matches 140; Conservative
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720383 GGGCTGCTGTTCACCTGCAACGGGCGCGGACGACGATGTTCGGGGTCACCGACCACGAC 720324
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  ) OTHER INFORMATION: CDC 1551
) OTHER INFORMATION: "n" bases at various positions throughout the sequence
) OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNS SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                        Length 4403765,
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Best Local Similarity 47.5%; Pred. No. 8.7;
Matches 112; Conservative 0; Mismatches 124;
                                                                                                                                                                                       0; Mismatches 124;
                                                                                                                                        DB 3;
                                                                                                                                        Score 37.6; DI
Pred. No. 8.7;
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
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US-09-328-352-1611
; Sequence 1611, Application US/09328352
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Patent No. 6294328
GENERAL INFORMATION:
                                                                                                                                  5.3%;
                                                                                                                                     Query Match
Best Local Similarity 47.59
Matches 112; Conservative
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LENGTH: 4411529
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Gaps
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Patent No. 6294328
GENERAL INFORMATION
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRAESK, Claire M.
APPLICANT: FRAESK, Claire M.
APPLICANT: FRAESK, Claire M.
TITLE OF INVENTION: DAS SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                    255 TGCCGTCATGGCAGCGAAAGACGCCATGACAAACAAGGTGGAAGCGCCACA 305
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                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
ITILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                         Sequence 15639, Application US/09621976 Patent No. 6639063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Ver. 2.1
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LENGTH: 4403765
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US-09-103-840A-2/c
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LENGTH: 505
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SOFTWARE:

TYPE: DNA

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APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
RIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1099
          Patent No. 6562958
GENERAL INFORMATION:
PREDICANT: GAZY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BUDGANAINI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 TGTTTTTAAAGGTTTAGGTATTGGTAGCGGCCTAATTGTAGCAATTGGTGCCCAAAATG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 TACTGGTGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCGGTTCTTCTCGTGTGTT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 CTTİTGİTCİRAAĞGĞARİĞĞĞÇİTAAAÇAĞÇAATATĞİRTİTĞĞİTATGİTİRATÇİĞİĞ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 cccigiccarrcaritiraricccrerdergrafiradrrificcgaaritardada 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 TCTTCATTACAGGICTGCTTTTGGGGGCCAGTCTTTTACTGTCCATCGGACCGCAGAATG
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4.9%; Score 35; DB 4; Length 1002;
Best Local Similarity 48.3%; Pred. No. 0.83;
Matches 131; Conservative 0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                               Query Match 5.0%; Score 35.4; DB 4; Length 636; Best Local Similarity 48.7%; Pred. No. 0.5; Matches 96; Conservative 0; Mismatches 101; Indels
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                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Pseudomonas aeruginosa
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; ORGANISM: Pseudo
US-09-252-991A-1099
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Sequence

Sequence 2624, App. Sequence 28428, A Sequence 1306, App. Sequence 1306, App. Sequence 119, App. Sequence 119, App. Sequence 119, App. Sequence 119, App. Sequence 119, App. Sequence 1320, Ap. Sequence 1332, A Sequence 1332, A Sequence 1332, A Sequence 14462, A Sequence 2510, App. Sequence 2510, App. Sequence 2510, Ap. Sequence 2510, Ap. Sequence 2510, Ap. Sequence 2510, Ap. Sequence 2510, Ap. Sequence 2510, Ap. Sequence 2510, Ap. Sequence 2510, Ap. Sequence 2510, Ap. Sequence 2510, Ap. Sequence 2510, Ap. Sequence 2510, Ap. Sequence 2510, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap. Sequence 26365, Ap

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1 atggtgatcatggaaatctt......aactgatgttgatgggttag 711
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

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Listing first 45 summaries
                                                             OM nucleic - nucleic search, using sw model
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ALIGNMENTS

1 AIGGIGALCAIGGAAAICTICAITACAGGICTGCTITTGGGGGCCAGTCTTTACIGICC 61 AICGGACGCCAGAAIGTACTGGIGAITAAACAAGGAATTAAGGAAGGACTCATTGCG	; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 7	, NUMBER OF SEQ ID NOS: 10	; PRIOR APPLICATION NUMBER: JP 2001-1777075 ; PRIOR FILING DATE: 2001-06-12	CURRENT FILING DATE: 2002-06-11	; FILE REFERENCE: 223789US	; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL; TITLE OF INVENTION: ASSIMILATING BACTERIUM
	j LENGTH: 711 j TYPE: DNA ORGANISM: Brevibacterium lactofermentum FRATURE: NAME/KRY: CDS LOCATION: (1)(711) OTHER INFORMATION: US-10-166-142-7 Query Match Best Local Similarity 100.0%; Score 711; DB 14; Length 711; Best Local Similarity 100.0%; Pred. No. 3.7e-225; Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	tentin version 3.1 revibacterium lactofermentum DS 11(711) MATION: 100.0%; Score 711; DB 14; Length 711; milarity 100.0%; Pred. No. 3.7e-225; Conservative 0; Mismatches 0; Indels 0; Gaps	Q ID NOS: 10 tentin version 3.1 revibacterium lactofermentum DS 11(711) MATION: 100.0%; Score 711; DB 14; Length 711; milarity 100.0%; Pred. No. 3.7e-225; Conservative 0; Mismatches 0; Indels 0; Gaps	ATION NUMBER: JP 2001-1777075 DATE: 2001-06-12 Q ID NOS: 10 tentin version 3.1 revibacterium lactofermentum DS 1)(711) MATION: milarity 100.0%; Score 711; DB 14; Length 711; milarity 100.0%; Pred. No. 3.7e-225; Conservative 0; Mismatches 0; Indels 0; Gaps	NG DATE: 2002-06-11 ATION NUMBER: 2002-06-11 ATION NUMBER: JP 2001-1777075 DATE: 2001-06-12 Q ID NOS: 10 tentIn version 3.1 revibacterium lactofermentum DS 11(711) MATION: milarity 100.0%; Score 711; DB 14; Length 711; milarity 100.0%; Pred. No. 3.7e-225; Conservative 0; Mismatches 0; Indels 0; Gaps	CE: 223789US CE: 223789US ICATION NUMBER: US/10/166,142 ANTION NUMBER: JP 2001-1777075 DATE: 2002-06-11 ANTION NUMBER: JP 2001-1777075 ANTION UNGS: 10 LentIn version 3.1 LentIn version 3.1 LentIn version 3.1 LentIn version 3.1 LentIn version 3.1 LentIn version 3.1 IOCO 08; Score 711; DB 14; Length 711; milarity 100.08; Pred. No. 3.7e-225; Conservative 0; Mismatches 0; Indels 0; Gaps
OV 1 AIGGIGATCATGGAAAATCTICATTACAGGICTGCTFTTIGGGGGCCAGTCTTTTACTGTCC 60	LENGTH: 711 TYPE: DNA O'SGANISM: Brevibacterium lactofermentum FBATURE: NAME/KEY: CDS LOCATION: (1)(711) O'THER INFORMATION: US-10-166-142-7	; SOTWARE: Patentin version 3.1 ; SOTWARE: Patentin version 3.1 ; TYPE: DNA ; TYPE: DNA ; ORGANIS: ; NAME/KEY: CDS ; LOCATION: (1) (711) ; OTHER INFORMATION: US-10-166-142-7	NUMBER OF SEQ ID NOS: 10 ; SOFTWARE: Patentin version 3.1 ; SOFTWARE: Patentin version 3.1 ; LENGTH: 711 ; TYPE: DNA ; ORGANISM: Brevibacterium lactofermentum ; FRATURE: ; NAME/KEY: CDS ; LOCATION: (1)(711) ; OTHER INFORMATION: US-10-166-142-7	; PRIOR APPLICATION WHORES: JP 2001-1777075 ; PRIOR PILING DATE: 2001-06-12 ; NUMBER OF SEQ ID NOS: 10 ; SOTHWARE: Patentin version 3.1 ; SEQ ID NO 7 ; LEWSTH: 71. ; TYPE: DNA ; ORGANISM: Bevibacterium lactofermentum ; REATURE: ; NAME/KEY: CDS ; LOCATION: (1) (711) ; GTHER INFORMATION: US-10-166-142-7	CURRENT FILING DATE: 2002-06-11 FRIOR APPLICATION NUMBER: JD 2001-1777075 FRIOR APPLICATION NUMBER: JP 2001-1777075 FRIOR FILING DATE: 2001-06-12 NUMBER OF SEQ ID NOS: 10 SOTHWARE: Patentin version 3.1 SEQ ID NO 7 SEQ ID NO 7 SEQ ID NO 7 FRATURE: ORGANISM: Brevibacterium lactofermentum FRATURE: NAME/KEY: CDS LOCATION: (1) (711) GTHER INFORMATION: US-10-166-142-7	FILE REFERENCE: 223769US CURRENT APPLICATION NUMBER: US/10/166,142 CURRENT FILING DATE: 2002-06-11 PRIOR APPLICATION NUMBER: US/201-1777075 PRIOR PILING DATE: 2001-06-12 NUMBER OF SEQ ID NOS: 10 SEQ ID NOS: 10 SEQ ID NOS: 10 LENGTH: 711 TYPE: DNA ORGANISM: Brevibacterium lactofermentum PEATURE: NAME/KEY: CDS JOSTON (1): (711) COTHER INFORMATION: US-10-166-142-7
<pre>Query Match 100.0%; Score 711; DB 14; Length 711; Best Local Similarity 100.0%; Pred. No. 3.7e-225; Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 1 ATGGTGATCATCATTACAGGTCTGCTTTTGGGGGCCAGTCTTTTACTGTCC 60</pre>	; LENGTH: 711 ; TYPE: DNA ; GRGANISM: Brevibacterium lactofermentum ; FRATURE:	; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 7; LENGTH: 71.1 ; TYPE: DNA; ; ORGANISM: Brevibacterium lactofermentum ; FRATURE:	NUMBER OF SEQ ID NOS: 10 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 7 ; LENGTH: 711 ; TYPE: DNA ; REWINSM: Brevibacterium lactofermentum ; FRATURE:	; PRIOR APPLICATION WUMBER: JP 2001-1777075 ; PRIOR FILING DATE: 2001-06-12 ; NUMBER OF SEQ ID NOS: 10 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 7 ; LEWSTH: 7.1 ; TYPE: DNA ; PRATURE:	CURRENT FILING DATE: 2002.06.11 PRIOR APPLICATION WUMBER: JP 2001-1777075 PRIOR PILING DATE: 2001-06-12 NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin version 3.1 SEQ ID NO 7 LEWSTH: 711 TYPE: DNA PRANTE: PROVIDACTOR IN BACCOFERMENTUM PRANTE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE	FILE REFERENCE: 223789US CURRENT APPLICATION NUMBER: US/10/166,142 CURRENT FILING DATE: 2002-06-11 PRIOR APPLICATION NUMBER: JP 2001-1777075 PRIOR FILING DATE: 2001-06-12 NUMBER OF SEQ ID NOS: 10 SOFTWARE: PatentIn version 3.1 SEQ ID NO 7 LENGTH: 711 TYPE: DNA ORGANISM: Brevibacterium lactofermentum FRATURE:
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ORGANISM: Brevibacterium lactofermentum ORGANISM: Brevibacterium lactofermentum FRAUTE: NAME/KEY: CDS LOCATION: (1)(711) OTHER INFORMATION: -10-166-142-7 LO-166-142-7 Beet Local Similarity 100.0%; Bred. No. 3.7e-225; Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 1 ATGSTGATCATGATAATGCAGTCTGCTTTTGGGGGCCAGTCTTTTACTGTCC 60		; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 7	; NUMBER OF SEQ ID NOS: 10 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 7	; PRIOR APPLICATION NUMBER: JP 2001-1777075 ; PRIOR FILING DATE: 2001-06-12 ; NUMBER OF SEQ ID NOS: 10 ; SOTTWARE: Patentin version 3.1 ; SEQ ID NO 7	CURRENT FILING DATE: 2002-06-11; PRIOR APPLICATION NUMBER: JP 2001-1777075 PRIOR FILING DATE: 2001-06-12; NUMBER OF SEQ ID NOS: 10 ; SOTTWARE: Patentin version 3.1	; FILE REFERENCE: 223789US ; CURRENT APPLICATION NUMBER: US/10/166,142 ; CURRENT FILING DATE: 2002-06-11 ; PRIOR APPLICATION NUMBER: JP 2001-1777075 ; PRIOR FILING DATE: 2001-06-12 ; NUMBER OF SEQ ID NOS: 10 ; SOCTWARE: PatentIn version 3.1 ; SEQ ID NO 7
S I O'M'E	; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL, ITILE OF INVENTION: ASSIMILATING BACTERIUM; FILE REPRENCE: 223789US; CURRENT APPLICATION NUMBER: US/10/166,142; CURRENT FILING DATE: 2002-06-11; PRIOR APPLICATION NUMBER: JP 2001-1777075; PRIOR APPLICATION NUMBER: JP 2001-1777075; NUMBER OF SEQ ID NOS: 10	; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL, ITILE OF INVENTION: ASSIMILATING BACTERIUM; FILE REFERENCE: 223789US; CURRENT APPLICATION NUMBER: US/10/166,142; CURRENT FILING DATE: 2002-06-11; PRIOR APPLICATION NUMBER: US/201-1777075; PRIOR PLILNG DATE: 2001-06-12	; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL; TITLE OF INVENTION: ASSIMILATING BACTERIUM; FILE REFERENCE: 223789US; CURRENT APPLICATION NUMBER: US/10/166,142; CURRENT FILING DATE: 2002-06-11	; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL; TITLE OF INVENTION: ASSIMILATING BACTERIUM ; FILE REFERENCE: 223789US . "TEDERM ADDITORATION MIMBED: IT 6/10/146 142	; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL; TITLE OF INVENTION: ASSIMILATING BACTERIUM	
S OME	APPLICANT: GNULY, YOSHHYA APPLICANT: YASUEDA, HISASHI TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL TITLE OF INVENTION: ASSIMILATING BACTERIUM FILLE REFERENCE: 223789US CURRENT APPLICATION NUMBER: US/10/166,142 CURRENT FILING DATE: 2002-06-11 PRIOR APPLICATION UNBER: JP 2001-1777075 NUMBER OF SEQ ID NOS: 10	; APPLICANT: GNULI, YOSHHYA ; APPLICANT: YASUBDA, HISASHI ; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL ; TITLE OF INVENTION: ASSIMILATING BACTERIUM ; FILE REFERENCE: 223789US ; CURRENT APPLICATION NUMBER: US/10/166,142 ; RIRENT FILING DATE: 2002-06-11 ; PRIOR APPLICATION UNMERR: US/201-1777075 ; PRIOR FILING DATE: 2001-06-12	; APPLICANT: GUNI, YOSHIYA ; APPLICANT: YASUBDA, HISASHI ; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL ; TITLE OF INVENTION: ASSIMILATING BACTERIUM ; FILLE REPREMENTE: 22399US ; CURRENT APPLICATION NUMBER: US/10/166,142 ; CURRENT FILING DATE: 2002-06-11	; APPLICANT: GUNII, YOSHIYA ; APPLICANT: YASUEDA, HISASHI ; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL ; TITLE OP INVENTION: ASSIMILATING BACTERIUM ; FILE RREFRENCE: 22789595 ; FILE REPERFENCE: 22789505	; APPLICANT: GUNII, YOSHIYA ; APPLICANT: YASUEDA, HISASHI ; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL ; TITLE OF INVENTION: ASSIMILATING BACTERIUM	; APPLICANT: GUNJI, YOSHIYA ; APPLICANT: YASUEDA, HISASHI
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N P P P P P P P P P P P P P P P P P P P	; Sequence 7, Application US/10166142 ; Publication No. US20030124687A1 ; GENERAL INFORMATION: APPLICANT: YASHDA, HISASH ; APPLICANT: YASHDA, HISASH ; TITLE OF INVENTION: ASSIMILATING BACTERIUM ; FILE REPERENCE: 2278959 ; CURRENT APPLICATION NUMBER: US/10/166,142 ; CURRENT FILING DATE: 2002-06-11 ; PRIOR APPLICATION NUMBER: UF 2001-1777075 ; PRIOR FILING DATE: 201-06-12 ; NUMBER OF SEQ ID NOS: 10	; Sequence 7, Application US/10166142 ; Publication No. US20030124687A1 ; GENERAL INFORMATION: ; APPLICANT: GUNJI, YOSHIYA ; APPLICANT: TASUEDA, HISASHI ; TITLE OF INVENTION: ASSIMILATING BACTERIUM ; FILLE OF INVENTION: ASSIMILATING BACTERIUM ; FILLE REPERBENCE: 22398048 ; CURRENT APPLICATION NUMBER: US/10/166,142 ; CURRENT FILING DATE: 2002-06-11 ; PRIOR APPLICATION UNMERR: US/2011-1777075	; Sequence 7, Application US/10166142 ; Publication No. US20030124687A1 ; GENERAL INFORMATION: ; APPLICANT: YASHEDA, HISASHI ; TITLE OF INVENTION: ASSIMILATING BACTERIUM ; FILLE OF INVENTION: ASSIMILATING BACTERIUM ; FILLE REPERENCE: 2278909 ; CURRENT APPLICATION NUMBER: US/10/166,142 ; CURRENT FILLING DATE: 2002-06-11	; Sequence 7, Application US/10166142 ; Publication No. US20030124687A1 ; GENERAL INFORMATION: APPLICANT: GUNJI, YOSHIYA ; APPLICANT: YASUBAA, HISASHI ; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL ; TITLE OP INVENTION: ASSIMILATING BACTERIUM ; FILLE REPREMENCE: 22798095 ; FILLE ARDERMENCE: 22798095	; Sequence 7, Application US/10166142 ; Publication No. US20030124687A1 ; GENERAL INFORMATION: ; APPLICANT: GUNJI, YOSHIYA ; APPLICANT: YASURDA, HISASHI ; TILLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL ; TITLE OF INVENTION: ASSIMILATING BACTERIUM	; Sequence 7, Application US/10166142 ; Publication No. US20030124687A1 ; GENERAL INFORMATION: ; APPLICANT: GUNJI, YOSHIYA ; APPLICANT: YASUEDA, HISASHI
i lough con i o i o i o i o i o i o i o i o i o i	US-10-166-142-7; Sequence 7, Application US/10166142; Sequence 7, Application NO. US20030124687A1; Sequence 7, Application No. US20030124687A1; Sequence 7, Application No. US20030124687A1; SensaAL INFORMATION: APPLICANT: GUNAI, YOSHIYA APPLICANT: ANGUEDA, HISASHI TITLE OF INVENTION: ASSIMILATING BACTERIUM FILLE REPERENCE: 22378908 CURRENT APPLICATION NUMBER: US/10/166,142 CURRENT FILING DATE: 2002-06-11 PRIOR APPLICATION UNMBER: UF 2001-1777075 PRIOR APPLICATION UNMBER: US/10/166,142 WUMBER OF SEQ ID NOS: 10	US-10-166-142-7 ; Sequence 7, Application US/10166142 ; Publication No. US20030124687A1 ; Publication No. US20030124687A1 ; GENERAL INFORMATION: ; APPLICANT: GUNI, YOSHIYA ; APPLICANT: GUNI, YOSHIYA ; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL ; TITLE OF INVENTION: ASSIMILATING BACTERIUM ; FILE REFERENCE: 22399US ; CURRENT APPLICATION NUMBER: US/10/166,142 ; CURRENT FILING DATE: 2002-06-11 ; PRIOR APPLICATION UNMBER: US/201-0777075	US-10-166-142-7; Sequence 7, Application US/10166142; Sequence 7, Application NO. US20030124687A1; Sequence 7, Application NO. US20030124687A1; Sequence 7, Application NO. US20030124687A1; SEDICAMT: GUNAI, YOSHIYA.; APPLICANT: GUNAI, YOSHIYA.; APPLICANT: YASUEDA, HISASHI.; TITLE OF INVENTION: ASSIMILATING BACTERIUM; FILLE REPERENCE: 2278789US; FILLE REPERENCE: 2278789US; CURRENT APPLICATION NUMBER: US/10/166,142; CURRENT FILING DATE: 2002-06-11	US-10-166-142-7; Sequence 7, Application US/10166142; Sequence 7, Application No. US20030124687A1; Jubilication No. US20030124687A1; APPLICANT: GUNJI, YOSHIYA APPLICANT: TASUBDA, HISASHIYA TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL; TITLE OF INVENTION: ASSIMILATING BACTERIUM FILLE OF INVENTION: ASSIMILATING BACTERIUM FILLE PREPERENCE: 223789US FILLE ARREPRENCE: 223789US	US-10-166-142-7 ; Sequence 7, Application US/10166142 ; Publication No. US20030124687A1 ; GENERAL INFORMATION: ; APPLICANT: GUNJI, YOSHIYA ; APPLICANT: YAGUEDA, HISASHI ; TILLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL ; TITLE OF INVENTION: ASSIMILATING BACTERIUM	US-10-166-142-7; Application US/10166142; Sequence 7, Application US/10166142; Publication WO. US20030124687A1; GENERAL INFORMATION: APPLICANT: GUNJI, YOSHIYA; APPLICANT: YASUEDA, HISASHI
α · α · α · · α · · α · · α · · α · · α · · α · · α · · α · · α · · · · · · · · · · · · · · · · · · · ·	RESULT 1 US-10-166-142-7 Sequence 7, Application US/10166142 Publication No. US20030124687A1 Publication No. US20030124687A1 Publication No. US20030124687A1 APPLICANT: GUNJI, YOSHYA APPLICANT: TANUEDA HISASHI TITLE OP INVENTION: ASSIMILATING BACTERIUM FILLE RERERENCE: 223789US CURRENT APPLICATION NUMBER: US/10/166,142 CURRENT FILING DATE: 2002-06-11 PRIOR APPLICATION UNBER: UP 2001-1777075 NUMBER OF SEQ IN NOS: 10	RESULT 1 US-10-166-142-7 Sequence 7, Application US/10166142 Publication No. US20030124687A1 Publication No. US20030124687A1 Publication No. US20030124687A1 APPLICANT: GUNI, YOSHYA APPLICANT: GUNI, YOSHYA TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL TITLE OF INVENTION: ASSIMILATING BACTERIUM FILE REPERBINGE: 22399US CURRENT FILING DATE: 2002-06-11 PRIOR APPLICATION UNMERR: US/10/166,142 PRIOR APPLICATION UNMERR: US/10/166,142 PRIOR FILING DATE: 2001-06-12	RESULT 1 US-10-166-142-7 Sequence 7, Application US/10166142 Publication No. US20030124687A1 JEBURAL INFORMATION: TITLE OF INVENTION: APPLICANT: ANSUEDA HISASHI TITLE OF INVENTION: ASSIMILATING BACTERIUM TITLE OF INVENTION: ASSIMILATING BACTERIUM FRIEBRE REPRESURE: 22789US CURRENT APPLICATION NUMBER: US/10/166,142 CURRENT FILING DATE: 2002-06-11	RESULT 1 US-10-166-142-7 Sequence 7, Application US/10166142 Sequence 7, Application No. US20030124687A1 Sebneral INFORMATION: APPLICANT: GUNJI, YOSHIYA APPLICANT: ASSIDEA HISASHI TITLE OF INVENTION: MSCHOOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL TITLE OF INVENTION: ASSIMILATING BACTERIUM FILLE REPERENCE: 2279789US FILLE REPERENCE: 2279789US	RESULT 1 US-10-166-142-7 ; Sequence 7, Application US/10166142 ; Publication No. US20030124687A1 ; GENERAL INFORMATION: ; APPLICANT: GUNJI, YOSHIYA ; APPLICANT: YASUBDA, HISASHI ; TILLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL ; TITLE OF INVENTION: ASSIMILATING BACTERIUM	RESULT 1 US-10-166-142-7 ; Sequence 7, Application US/10166142 ; Publication No. US20030124687A1 ; GENERAL INFORMATION: ; APPLICANT: GUNJI, YOSHIYA ; APPLICANT: YASUEDA, HISASHI

Sequence 7, Appli Sequence 51, Appl Sequence 14, Appl Sequence 14, Appli Sequence 9, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appl Sequence 648, Appl Sequence 648, Appl Sequence 5949, Appli Sequence 549, Appli Sequence 31368, Appli Sequence 31368, Appli Sequence 31368, Appli Sequence 31368, Appli Sequence 31368, Appli

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100.0%; Pred. No. 4e-225;
ive 0; Mismatches 0
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; Sequence 24, Application US/10196232
; Publication No. US20030113899A1
; GENERAL INFORMATION
; APPLICANT: YANAGUGHI, MIKIKO
; APPLICANT: ITO, HISAO
; APPLICANT: GUNJI, YOSHIYA
                                                                          TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
                                                                                                                                                                                                                    Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 711; Conservative 0
NUMBER OF SEQ ID NOS: 125
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 51
LENGTH: 922
                                                                                                                                             ; LOCATION: (101)..(799)
; OTHER INFORMATION: RXA01394
US-09-746-660A-51
                                                                                                                                NAME/KEY: CDS
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                            GATCITTTGTCCAATGCCGCGCCGATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCT
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APPLICANT: Zelder, Osker
APPLICANT: Zelder, Osker
APPLICANT: Reberhauer, Gregor
APPLICANT: Lee, Heung-Schick
APPLICANT: Lee, Heung-Schick
APPLICANT: Heang, BAUING-JOON
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CP2
CURRENT APPLICATION WHOBER: US/09/746,660A
CURRENT FILING DATE: 2000-12-22
PRIOR PELICATION NUMBER: 09/603124
PRIOR PELICATION NUMBER: 09/603124
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142101
PRIOR FILING DATE: 1999-07-02
PRIOR PELICATION NUMBER: 60/148613
PRIOR FILING DATE: 1999-07-02
PRIOR PELICATION NUMBER: 60/148613
PRIOR PELICATION NUMBER: 60/148613
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; Sequence 51, Application US/09746660A
; Publication No. US20030049804A1
; GENERAL INFORMATION:
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APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
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TITLE OF INVENTION: METHOD FOR PRODUCING L-ARGININE
FILE REPERRINCE: 225391USO
CURRENT APPLICATION NUMBER: US/10/196,232
CURRENT FILING DATE: 2002-07-17
FPRIOR PILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
LENGTH: 2374
                                                                                                                                                                                                                                                               100.0%; Score 711; DB 14;
100.0%; Pred. No. 6.7e-225;
tive 0; Mismatches 0;
                                                                                                                                                            ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 711, Conservative
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US-10-196-232-24
                                                                                                                                                                                         NAME/KEY: CDS
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RESULT

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APPLICANT: ICEDA, MAGATO
TILLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFREENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT PILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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Sequence 1, Application US/09738626
Publication No. US20020197605A1
                                                                                             APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                           HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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Best Local Similarity 100.0
Matches 711; Conservative
                                                                         GENERAL INFORMATION
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Sequence 9, Application US/10166142
; Sequence 9, Application US/10166142
; Publication No. US20030124687A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: GUNI, YOSHIYA
; APPLICANT: GINI, YOSHIYA
; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL
; TITLE OF INVENTION: ASSIMILATING BACTERIUM
; FILE REFERENCE: 223789US
; CURRENT APPLICATION NUMBER: US/10/166,142
; CURRENT APPLICATION NUMBER: US 2002-06-11
; PRIOR APPLICATION NUMBER: LP 2001-1777075
; RIGHER FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 9
; LENGTH, 712
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                                                                                                                                                                              GCGGTGGCCACTGACACGCGCAACCGGGTGCGGGTGAGCGTCGAGCGTCGATAAGCAGCGG
                                                                                                                                                       TTGGACGCGTTTGTGTTTTATCGGCGCGTCGGCGCGCAATACGGCGACACCGGTGG
                               361 éCGGTGGCCACTGACACGCGCAACCGGGTGCGGCTGGAGGTGAGCGTCGATAAGCAGCGG
                                                                             GTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                       661 GIGGCAGIIGIGAIGACCGCAIIGGCCAICAAACIGAIGIIGAIGGGI 708
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LOCATION: (1)..(375)
OTHER INFORMATION:
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US-10-166-142-9
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1328413 ATTITICGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGC 1328354
                                                                                              1328353 GCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTC 1328294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAAGCGCGAAGGACTCATTGCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OCHIAL, KRIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CUNRENT FILINO BATE: 2000-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PELICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                               Sequence 3455, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Corynebacterium glutamicum
US-09-738-626-3455
                                                                                                                                                                                                                                                                                                                                                             MIZOGUCHI, HIROSHI
ANDO, SELTKO
HAYASHI, MIKRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NOOKO
SENOH, AKIHIRO
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APPLICANT:
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                                          406 GCTCGATCGCGGCCGGCCGCCTCACTGCGCTGGACCTTCGGTCTCGGCGCGCCCTTC 465
                                                                                                                                                                                    625 TCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTGGCAGTTGTGATGACCGCATTG 684
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       505 GCCTCGCCCCAATACGCCGACACACGGTGGATTTTCGCCGCTGGCGTTCGCG 564
                                                                                              565 GCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGCGCAGCAGCATTGTCACGCCCGCTG 624
                                                                                                                                        466 GCGAGCCTGTGCTGGTTCGCCGCCTCGGCTTCGGCTCACGGCTGCTCGGCCGCTTCCTG 525
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; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UUN
APPLICANT: HORINAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: BALTOKI, MASHIRA
TILLE OF INVENTION'I MASHIRA
TILLE OF INVENTION'I MASHIRA
TILLE OF INVENTION'I NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
FRIOR FILING DATE: 2001-05-30
FRIOR FILING DATE: 2001-05-30
FRIOR FILING DATE: 2001-05-30
FRIOR FILING DATE: 2001-06-30
FRIOR FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10156761
Publication No. US20030119018A1
GABREAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
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US-10-156-761-1/c
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                                                                                                                                   GGCGGTGGCCACTGACACGCGCAACCGGGTGCGGGTGAGGTGAGCGTCGATAAGCAGCG 419
                                                                                                                                                                    GGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTA 479
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                                            CCACAGATCATTGAAGAAACAGAACCAACCGTGCCCGATGACACGCCTTTGGGCG-GTTC
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Pred. No. 4.7e-10;
0; Mismatches 147; Indels 3
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Publication No. US2003011901841
GENERAL INFORMATION
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIGAMA, UUN
APPLICANT: ISHIGAMA, UUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKT, VOSHIVIKI
APPLICANT: BARTAMA, UND
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UF 2001-204089
PRIOR APPLICATION NUMBER: UF 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2010-06-02
NUMBER OF SEQ ID NOS: 15109
LENGTH: 609
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Query Match
Best Local Similarity 52.2%
Matches 164; Conservative
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US-10-156-761-1109
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US-10-156-761-1109
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APPLICANT: Behr, Marcel
APPLICANT: Behr, Marcel
APPLICANT: Small, Petex
APPLICANT: Schoolin, Gary
APPLICANT: Schoolin, Gary
APPLICANT: Schoolin, Gary
APPLICANT: Wilson, Michael A.
TITLE OF INVENTION: Molecular Differences Between Species of
TITLE OF INVENTION: Molecular Differences Between Species of
TITLE OF INVENTION: Molecular Differences Between Species of
TITLE OF INVENTION: Molecular Differences Between Species of
TITLE OF INVENTION: MOLECULAR DATE: US/09/894,844
CURRENT APPLICATION NUMBER: US/09/894,844
CURRENT FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-08-25
PRIOR PILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: FastSEQ for Windows Version 4.0
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| Publication No. US20040018574A1
| GENERAL INFORMATION:
| APPLICANT: Behr, Marcel
| APPLICANT: Small, Peter
| APPLICANT: Schoolnik, Gary
| APPLICANT: Schoolnik, Gary
| TITLE OF INVENTION: Michael N. Tuberculosis Complex
| TITLE OF INVENTION: the M. Tuberculosis Complex
| TITLE OF INVENTION: the M. Tuberculosis Complex
| TITLE OF INVENTION WOMERR: US/10/388,902
| CURRENT FILING DATE: 2003-03-14
| PRIOR APPLICATION NUMBER: US/09/894,844
| PRIOR APPLICATION NUMBER: 09/318,191
| PRIOR FILING DATE: 1999-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.0%; Score 57; DB 9; Length 597; Best Local Similarity 53.1%; Pred. No. 3.9e-08; Matches 145; Conservative 0; Mismatches 125; Indels
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                                                                                                                                                                                                                                                             Sequence 11, Application US/09894844; Patent No. US20020176873A1; GENERAL INFORMATION:
RESULT 10
US-10-388-902-11
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SEQ ID NO 11
LENGTH: 597
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TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR

TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR

TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

FILE REFERENCE: 03495.0218

FILE REFERENCE: 03495.0218

CURRENT APPLICATION WHOBER: US/10/080,170

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION UNMBER: 60/270,123

PRIOR APPLICATION UNMBER: 60/270,123

NUMBER: OF SEQ ID NOS: 652

SOFTWARE: PATENTIN Ver. 2.1
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Best Local Similarity 53.1%; Pred. No. 3.9e-08,
Matches 145; Conservative 0; Manatches 125; Indels
Matches 145; Conservative 0; Manatches 125; Indels
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PRIOR APPLICATION NUMBER: 60/097,936
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 597
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US-10-080-170-648
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US-10-388-902-11
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Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: DAMPER: US 06)369,493
CURRENT FILING DAMPE: 2003-02-28
FRIOR PREJING DAMPE: 2003-02-28
FRIOR PREJING DAMPE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
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l Similarity 51.1%; Pred. No. 0.019;
95; Conservative 0; Mismatches 91; Indels 0;
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     ; FILE REFERENCE: 249-262
; CURRENT PAPPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: UP 2001-204089
; PRIOR PLING DATE: 2001-05-30
; PRIOR FILING DATE: 2001-08-02
; PRIOR FILING DATE: 2010-08-02
; SEQ ID NO 1
; SEQ ID NO 1
; LENGTH: 9025608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Streptomyces avermitilis
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ORGANISM: Burkholderia cepacia
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Matches 95; Conserv
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US-10-369-493-31368
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617 GCCCGCTGTCCAGCCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGCAGTTGTGATGA
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APPLICANT: IKEDA, HARUO
APPLICANT: SHIRAWA, JUN
APPLICANT: HORIKAWA, JUN
APPLICANT: HORIKAWA, HROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAXI, YOSHTYUKI
APPLICANT: BATTORI, MASAHIRA
TILLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR PHILNG DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PHILNG DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PHILNG DATE: 2001-06-02
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWIRA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHEMA, TADAYOSHI
APPLICANT: SARAKI, YOSHIVUKI
APPLICANT: SARAKI, YOSHIVUKI
APPLICANT: HATOSHI, WASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                            677 CCGCATTGGCCATCAAACTGATGTTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5949, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
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US-10-156-761-5949
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LENGTH: 3000
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US-10-156-761-1
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Sequence 28610, Application US/10369493
| Publication No. US2003023675A1
| Publication No. US2003023675A1
| GENERAL INFORMATION:
| APPLICANT: Hinkle, Gregory J.
| APPLICANT: Stater, Steven C.
| APPLICANT: Goldman, Barry S.
| APPLICANT: Chen, Xianfeng |
| TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERING IN PLANTS FOR PRODUCTION OF ITTLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES
| FILE REFERENCE: 38-10(52052) B |
| CURRENT FILING DATE: 2003-02-28 |
| PRIOR APPLICATION NUMBER: US/10/369,493 |
| CURRENT FILING DATE: 2002-02-21 |
| NUMBER OF SEQ ID NOS: 47374 |
| SEQ ID NO 28610 |
| LENGTH: 1443 |
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  843 CATITICGICGCGGCCGCTGIACGAAGCGIICGICGCCCAAIACAGCGACGCCGICAA 902
                                                                                                 903 GGCGCTGAAAGTCGGCGCTGCGTTCGAAGCGAACGTGGAACGTCGGCCCGTTGATGCATCA 962
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                                                   GTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGGCTGGGTTT 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: March 17, 2004, 09:46:58 Job time : 282.891 secs
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ORGANISM: Burkholderia fungorum
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963 AGCCGC 968
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38.2	ALIGNMENTS			AL151258 AL151258 GSS.	≨	Anopheles. Anopheles. 1 (bases 1 to 830) Genoscope. Direct Submission	<pre>JURNAL Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.qenoscope.cns.fr)</pre>		DURNAL Submitted (16-FEBS-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France ROUX, Paris 75015, France This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the
	13:43:00 ; Search time 1955.25 Seconds (without alignments) 10858.975 Million cell updates/sec	_COPY_1016_1726 c c c c c c aactgatgttgatgggttag 711 c c c c c c c c c c c c c c c c c c	apext 1.0 14931090276 residues	hits satisfying chosen parameters: 55026578 c 25		% 00% IS summaries					* * *			ACCESSION 0;* VERSION d:* KEYWORDS	08	er of results predicted by chance to have a REFERENCE equal to the score of the result being printed, AUTHORS TITLE TITLE	1	ID Description	29 CNSO1MOH AL151258 Anopheles JOURNAL BZ554294 BZ554294 pacell 60 28 BZ5560550 BZ560550 pace2-164 COMMENT 28 BZ568946 BZ568946 pace2-164
Copyright (15, 200		Scoring table: IDENTITY NUC Gapop 10.0 , G Searched: 27513289 segs,	umber of	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match (Maximum Match 1	SI	3: em_estin:* 4: em_estin:* 5: em_estov:* 6: em_estyl:*	7: em_estro:* 8: em_htc:* 9: qb_est1:*	10: 9b est2:4 11: 9b htc:* 12: 9b est3:*	13: gb_eet4:* 14: gb_eet5:* 15: em eetfun:* 16: em eetfun:*	17: em_gss_hum:* 18: em_gss_inv:* 10: em_gss_inv:*	em 988	666	26: em gss phg:* 27: em gss vrl:* 28: gb_gssl:* 29: gb_gss2:*	L m €	ر مد	Sult Query No. Score Match Length I	c 1 60.4 8.5 830 c 3 54.2 7.6 893 c 4 51.4 7.2 1620

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pacs2-164_2569.x1 pacs2-164 Pseudomonas aeruginosa genomic clone pacs2-164_2569, genomic survey sequence.
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aerteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadacae, Pseudomonas.
( (bases 1 to 897)
                                                                                                                                                            7 ATCATGGAAATCTTCATTACAGGTCTGCTTTTGGGGGCCAGTCTTTACTGTCCATCGGA
                                                                                                                                                                                                                                                                                                                                     127 CTCGTGTGTTTAATTTCTGACGTCTTTTTTGTTCATCGCCGGCACCTTGGGCGTTGATCTT
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Burns,J.L., Kaul,R. and Olsen,M.V.
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|Clone="pacs2-164" 2569"
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|mote="clinical isolate 2-164 Whole genomic shotgun
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Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
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                                                                     Query Match 8.0%; Score 56.8; DB 28; Length 1034; Best Local Similarity 50.4%; Pred. No. 0.0009; Matches 139; Conservative 0; Mismatches 137; Indels 0;
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University of Washington
University of Washington
Fox 352145, Seattle, WA 98105-2145, US
Fox: 2062316954
Fax: 2066857244
Email: craymond@u.washington.edu
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/strain="2-164"
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         library."
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KEYWORDS
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Burns, J.L., Kaul, R. and Olsen, M.V.

Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press

Contact: Chris K. Raymond
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                                                                                                                                                                                                                                                                                                                                                                       23 TTACAGGTCTGCTTTTGGGGGCCAGTCTTTTACTGTCCATCGGACCGCAGAATGTACTGG
                                                                                                                                                                                                                                                                                                                                       Gaps
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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/clone="pacs1-60 4617"
/clone lib="pacs1-60"
/note="clinical isolate 1-60 Whole genomic shotgun
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0
                                                                                                                                                                                                                                                                                         Length 830;
                                                                                                                                                                                                                                                                                                                              1; Mismatches 137; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 GCGCCTGAAACGGCGATGAGCAGTAACCTCGAACTGGC 318
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                                                                                                                                                                                                                                                                                    8.5%; Score 60.4; DB 29; 50.7%; Pred. No. 9.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216554
Fax: 2066857244
Email: craymond@u.washington.edu
                                                       1. .830
/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
                                                                                                                                                 /db xref="taxon:7165"
/clone="22E24"
/clone_lib="NotreDame1"
/note="end : T7"
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/strain="1-60"
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/organism="Pseudomonas
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1 (bases 1 to 1034)
                                         Location/Qualifiers
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Pseudomonas aeruginosa
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                                       FEATURES
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GSS 17-DEC-2002
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Burns, J. L., Kaul, R. and Olsen, M.V.
Burns, J. L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sacquence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
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Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 TTACTGTCCATCGGACGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAGGA 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 CTCATTGCGGTTCTTCTGGGGTTTTAATTTCTGAGGTCTTTTTGTTCATCGCCGGCACC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                  BZ556963 833 bp DNA linear GSS 17-DBC-pacs1-60_5975.x1 pacs1-60 Pseudomonas aeruginosa genomic clone
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/clone="pacs1-60 5975"
/clone-lib="pacs1-60"
/clone-lib="pacs1-60"
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50.6%; Pred. No. 0.12;
tive 0; Mismatches 114;
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GSS.
Drosophila melanogaster (fruit fly)
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/strain="1-60"
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          438 GATA 435
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          559
                                                                                                                            560 TCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGCGCAGCAATTGTCACGCC 619
                                                                                                                                                                                                                                                                620 CGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGCAGTTGTGATGACCG 679
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                                                            492 GGTTCGCTCGGCCCCAGCAGACCCCCC-----CCCCCCCCTTATGCCCTCCGCCGC 441
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Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1620)
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Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
500 TCGGCGGCGTCGGCGCGCAATACGGCGACACCCGGACGGTGGATTTTCGCCGCTGGCGCGT
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/clone="pacs2-164_8165"
/clone lib="pacs2-164"
/clone lib="pacs2-164"
library."
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Pred. No. 0.027;
0; Mismatches 84; Indels 0;
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Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                           320 GCAIGGCCGCGCAACTGCTGTTCCGGGGATA 290
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/strain="2-164"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        craymond@u.washington.edu
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Contact: Chris K. Raymond
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University of Washington
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Best Local Similarity 54.3%;
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Email: craymond
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BZ568946/c
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Zea mays
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                 URL :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 CIGACGICITITIGIICAICGCCGGCACCIIGGGCGIIGAICIIIIIGICCAAIGCCGCGC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 CGATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCTTACCTGTTATGGTTTGCCGTCA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 ---TGGCAGCGAAAGACGCCATGACAAACAAGTGGAAGCGCCACAGATCATTGAAGAAA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 CAGAACCAACCGIGCCCGAIGACACGCCITITGGGCGGITCGGCGGTGGCCACTGACACGC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Homo sapiens NEUROBLASTOWA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                       Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Libraris was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com U
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODCOOLAbO4QPI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
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                                                                                                             Li.W.B. Gruber.C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.7%; Score 47.6; DB 13; 17.2%; Pred. No. 0.22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/clone="CS0DC001YG07"
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                                                                                                                                                                                                                                                                    - Web: www.genoscope.com.france.com.genoscope.com.france.com.genoscope.com.france.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.genoscope.com.
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BX393687
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                                                                                                                                                                                                                Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 CCAACCGTGCCCGATGACACGCCTTTGGGCGGTTCGGCGGTGGCCACTGACACGCGCAAC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        565 GCAAGCCIGAICTGGTICCCGCTGGTGGGTITTGGGCGCAGCAGCATGTCACGCCCGCTG 624
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                                Eukaryota, Metaroa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 925)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 157; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
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      Drosophila melanogaster
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Query Match

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 620)
                                                                                                                                                                                                                        Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr)
                                                Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405 CGTCGATAAGCAGCGGGTTTGGGTAAAGCCCCATGTTGATGGCAATCGTGCTGACCTGGTT
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llarity 48.1%; Pred. No. 0.54;
Conservative 0; Mismatches 140; Indels
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Email: walbot@stanford.edu
Plate: 1114036 row: D column: 07.
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Contact: Walbot V
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Pooideae; Triticeae; Triticum.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                        Department of Biological Sciences
Stanford University
SES California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: walbot@stanford.edu
Plate: 1117004 row: E column: 09.
Location/Qualifiers
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Gaps

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AM927407
945001E08.X1 945 - Mixed adult tissues from Walbot lab, same as 707
(SK) Zea mays cDNA, mRNA sequence.
                                                                                                                                                      /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between Imm and Jame. Sharon Stanfield prepared the CDNA lobrary in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
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Fax: 650 725 8221
Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                      Query Match 6.2%; Score 44.4; DB 13; Best Local Similarity 46.0%; Pred. No. 1.4; Matches 150; Conservative 0; Mismatches 176;
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Plate: 945001 row: E column: 08.
Location/Qualifiers
1. .532
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/mol_type="mRNA"
/cultivar="0H43"
/db_xref="taxon:4577"
/tissue_type="tassels"
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Contact: Walbot V
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Pred. No. 1.4;
0; Mismatches 176; Indels 0
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Department of Biological Sciences
Stanford University
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Plate: 946110 row: C column:
Location/Qualifiers
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/ organism="Homo sapiens"

/mol_type="mRNA"

/mol_type="mRNA"

/mol_type="mRNA"

/bore="ctoBe022xA07"

/tissue type="NEUROBLASTOWA"

/clone lib="Homo sapiens NEUROBLASTOMA"

/note="Vector: porNSPORT 6; let strand cDNA was primed

/note="Vector: porNSPORT 6; let strand cDNA was primed

with a NotI-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned into

the Not I and BCORV sites of the pCMVSPORT 6 vector.

Library was not normalized."
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Extravora: Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Bakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria; Primates, Catarrhini; Hominidae, Homo.

E 1 (bases 1 to 885)
Is Liw.B. (Stuber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
L Unpublished (2001)
Contact: Genoscope
Centre National de Sequencage
Genoscope - Centre National
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Inbrary was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies.
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.hrvitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBBO22ZAO7FPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX425603 885 bp mRNA linear EST 15-MAY-2003 BX425603 Homo sapiens NBUROBLASTOMA Homo sapiens cDNA clone CLOBB022ZA07 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                   405 CGTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTT 464
                                                                                                                                                                                                                                                                                                                                                                                  465 GAACCCGAATGCGTATTTGGACGCGTTTGTGTTTATCGGCGCGTCGGCGCGCAATACGG 524
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0
                                                                                                                                                                                                                               6.0%; Score 42.8; DB 14; Length Similarity 47.4%; Pred. No. 3.4; Conservative 0; Mismatches 142; Indels
organism="Triticum aestivum"
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                   /mol_type="mRNA"
cultivar="recital"
/db_xref="texxon:4565"
/clone="AZO1101N14"
/tissue_type="leaf"
/clone_lib="AZO1"
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AZOI.101N14F010125 AZOI Triticum aestivum cDNA clone AZO1101N14,
mRNA sequence.
                                                                                                                                                                                                                                       Junce="Organ: Tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoR1; cDNA library from fully
differentiated maize Lissues from an active Mutator plant.
Tissue ratio 18 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
1 (bases 1 to 538)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 TIGGGCGGTTCGGCGGTGGCCACTGACACGCGCAACCGGGTGCGGGTGAGGTGAGCGTC 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 CTCTCGTAGTAGACGAGGTGGAGCGAAGTGGACGTAGCAGGTGCCGGCGAGGTGGATC 213
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                                                                                                   /tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev stage="fully-grown"
/lab_host="DH108"
                                                                                                                                                                             /clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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                                                                                     /db xref="taxon:4577"
           organism="Zea mays"
                                 /mol_type="mRNA"
/cultivar="W23"
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- Web: www.genoscope.cns. It.

- Web: www.genoscope.cns. It.

- Determination of this BAC-end sequence was carried out as part of betermination with the Berkelsy Drosophila Genome Project (BDGP).

- Collaboration with the Berkelsy Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and maranogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecognic strain v2; on bw 5p, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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survey sequence T7 end of BAC #
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                           0; Gaps
h
Similarity 0.9%; Pred. No. 7.3;
4; Conservative 141; Mismatches 279; Indels
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melanogaster"
                                                                                                                                     Similarity 14.8%; Score 41.2; DB 29; Similarity 14.8%; Pred. No. 11; Conservative 150; Mismatches 119;
             /mol_type="genomic DNA"
/db xref="texon:7227"
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organism="Drosophila"
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1 gtcgataagcagcgggtttg......tggtgagctctggaccgtag 873
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		X96471 C.glutamicu A93933 Sequence 2	Coryneb	Ŝ	Seque	BD165655 Novel pol	Seque	AX067087 Sequence	AFUUSZIG COLYMEDAC	AX244059 Sequence	AX643028 Sequence	AX643030 Sequence	AX123539 Sequence	BD165656 Novel pol	BX248357 Corynebac	ABOR1133 Corynebac	AP003001 Mesorhizo	AE008076 Agrobacte	AE009111 Agrobacte	ALSS132 Screpcomp ALS91788 Sinorhizo	AP005025 Streptomy	AE011965 Xanthomon	AL939131 Strepcomy M37389 Pseudomonas	AE002063 Deinococc	AE005530 Escherich	AE015317 Shigella	AE016988 Shigella	AE016766 Escherich	AE000382 Escherich	ACOSORRA MUS MUSCU	1 1	N	835	. .	937	2071 Sequenc	25196 Sequence	38653		linear BCT 19-MAR-2001	Š		regulator protein; Lysine		idae; Actinomycetales; Corynebacterium.	•	type of cellular function:
SUMMARIES	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SZ	A44443 *********************************	AF0032//	AX123538	BD165655	AX813971	AX067087	AP005218	AX063771	AXZ44059 AY643028	AX643030	AX123539	BD165656	BX248357	E54483	AB083133 AD003001	AE008076	AE009111	SC0939132	AP005025	AE011965	SC0939131	AE002063	AE005530	AE015317	AP002563	AE016766	AE000382	ECU28377	AC020884 U	AL627274	AE016835	AE008808	AL646059	AE016937	AR025196	AR038653	ALIGNMENTS		2374 bp DNA and lysG genes.	1	; Lysine export	ง ซี สิ	gintamicum bacteria; Actinobacteridae; e: Commebacteriaceae; Cory		m,H. and Eggeling,L. transporter with a new t)
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Vrlijc,M. and Eggeling,L.
PROCESS FOR THE NICROBIAL PRODUCTION OF AMINO ACIDS ACTIVITY OF EXPORT CARRIERS
PACENT: WO 9723597-A 2 03-JUL-1997;
KERNFORSCHUNGSANLAGE JUELICH (DE); VRLIJC MARINA (DE
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ETEPTVEDDFLEGGSAVATOTRNKVRYEVSVDKQRVWKRMLMAIVLTWIANENALDA
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SYPEQLDNSLOSINNIEFSDAELEAIDBISHDAGINIWAKATDSKTREN"
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AEGFGBAIRRGLGWGLLPETQAAPMLKAGEVILLDEIPIDTPMYWQRWRLESRSLARL
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                                                                                                                             Submitted (07-MAR-1996) M.M. Vrljic, Institut fuer Biotechnologie
1, Forschungszentrum Juelich, Postfach 1913, D-52425 Juelich, FRG
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                      regulator protein"
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   from Corynebacterium glutamicum 22 (5), 815-826 (1996)
                                                                                                                                                                                               /organism="Corynebacterium glutamicum"
/mol_type="genomic DNA"
/straft27"
/db xref="taxon:1718"
complement(82. .954)
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/trans1_table=11
product="Lysine exporter protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GOA:P94632"
/db_xref="SWISS-PROT:P94632"
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/protein_id="CAA65323.1"
/db_xref="GI:1729754"
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|db_xref="GI:13397387"
|db_xref="GOA:P94633"
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protein id="CAA65325.1"
db_xref="GI:1729756"
                                                                                                                                                                                                                                                                                                                              gene="lysg"
note="Lysine governor"
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/gene="lysE"
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Vrljic,M.M.
Direct Submission
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KEYWORDS
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                      1. .2374
/organism="Corynebacterium glutamicum"
/mol_type="unassigned DNA"
/db_xref="taxon:1718"
                                                                                                                                                                  100.0%; Score 873; DB 6; L
100.0%; Pred. No. 9.8e-185;
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    Location/Qualifiers
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RESULT 3

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AP005277 333150 bp DNA linear BCT 08-AUG-2002 Corynebacterium glutamicum ATCC 13032 DNA, complete genome, section
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Filallvpirragskipoaaltgwylrotsrskywyigsngofysalgigvaalfirg
Walgitviyllaalslfrsmcsiaskdvoggkviskgkrgivtgratviggymglvagl
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BPQDRTTLAIGPGERWEI VYELEPGEDVTLESVGFEDNYGFSDDDEFVPDFGMSDSFGL
LITITGPSDDAAQAPLAF DGVLLVRFTSEDVUI DATERTFINNTFSINDLQMDMGRVVVID
HDQPSWAIVTNINSDWFHNFHYIDARFYVLKFEGTDVELFUGWKOTVGLEPGARTATL
AVEFGHYDDPQMPYMYHGHMLXHEDQGMMGQFVI VEFGDERAAVLGSGTGSSIDSAGG
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DVINNLDEMTTVHWHGMKLPALADGGPHSPIGPGQTWSPTWTVANDAATLWYHPHTHG
                                                                                                                                                                                                                                                                              Complete genomic sequence of Corynebacterium glutamicum ATCC 13032
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MPELNRRTFFKGAGVLAATVVGAQVLVACSSDDVRGYGGEPRTL"
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                                                                                                                                                                                                                                                                                                                                                           /gene="Cgl0946"
/note="PF00005:ABC transporter
TIGR00960:3a0501802: Type II (General) Secretory Pathway
                                                                                                                                  Corynebacterium glutamicum ATCC 13032
Corynebacterium glutamicum ATCC 13032
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                             Corynebacterineae; Corynebacteriaceae; Corynebacterium
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/product="Purative multicopper oxidases"
/protein id="RAB9838.1"
/db_xref="G1:21323712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Hypothetical me
/protein_id="BAB98337.1"
/db_xref="GI:21323711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
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1382. .2917
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AP005277 BA000036
AP005277.1 GI:21323710
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3063. .3983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (63
                                                                                                                                                                                                                                                                                                                          (bases 1 to 333150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3063. 3983
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328478 GACACCGGACGGTGGATTTTCGCCGCTGGCGCTTCGCGGCAAGCCTGATCTGGTTCCCG 328419
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GLIVUHAVITKOLRRILVVGIJVAFVVLEPESTREGSRALNRAVNFESHALRVEVBAD
HALKNLDPRNILVPGEWARSREJADADSSTR.FEGOJGTGVGSAATVLLEGBATYLLIEDNILV
GLIVILVILVPI ISQVVALASKGI SKRSVTQCBKLASGGAGASDIMMGLRVIKALGGERN
AVKTPEKASGARRANVDTANASGKVAGIGELSIAVNLAAVLLIAGMRVTTGGELGFGO
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FULVIRVPRASTLEHGDNILATPHAADI FEGTLRSNISMNHEDNVPI DPQVIRASGLTDI
IEVDGLIDAPVRDTGSNILGGGGRQRVALARALHADAEVLVLMDFTSAVDSVTEVSITAQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LASISSTELLINUYRDENNQYVPEDQSHYVNGYIDSIAGSAAAGQUGYAVGYITALMTSS
AYVRAFSRCANAVYGRSEGRILIKRMAMLLFINLALLIGIIIILUSWYLNETLUWGIF
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//gene="rg10952"
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DPSNRTDVCVLDLOLGGIDGIDTATRLMBTTPDLAVLI VTSHARPROLKRALAAGVLG
FLPKTSTADBFATAIRTVHAGRRYIDPELAAMTISAGESPLTNREEEVLELAGGGLSA
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SGDRKERLNFQGWKYALNRTVRDVFPDGLLDLAALLTFFSILSIAPAVLLGYSVITIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MMRTTHTASSILRRMIRRQRGKVAFGAFFLGMWQLSEALVPIAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 CTGGTGGGTTTTCGGCGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACCCGAATGCGTATTTGGACGCGTTTGTGTTTATCGGCGGCGTCGGCGCGCAATACGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GICGATAAGCAGCGGGTTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="ABC-type multidrug/protein/lipid transport
system, ATPase component"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 333150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00664;ABC transporter transmembrane region."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transI table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 7.7e-185;
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                                                                                                                                                                                                                                                product="Hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="Cg10952"
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                                                                                                                                                                                                                                                                                                                                                                        WIGL PRETFVPAFVGSTVLAVLSF
                                                                                                                                         complement(6781. ,6987)
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                                                                                     complement (6781. .6987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'db xref="GI:21323718"
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10107, ,11843
                                                                                                                                                                                                                              trans table=11
                                                                                                                                                                                                                                                                                                                                                                                                   .048. .8205
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transl_table=
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trans1 table=
                                                                                                                                                                                              codon start=1
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ilarity 100.0%;
Conservative 0
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Best Local S:
Matches 873,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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PWANYRWVWLIAMSAVLWWTSTTDYLSALWVVIPPLMAGTVRLSVWTVDVMKEVERS
RELEASLRVTEERLIERARGEHDTLGGHLAAMSVKSELALAARGBOERBEIRBLGK
LTRTSMSEMRDVVSGYRTVMLATEIEGAKSLLADAHIHLSVLGTSGVSFAHRELCAL
LVREATTWLIAEDAPDATLTLSSTEVRMDNNGVNKDIGRLSGLSALRSRAESAGWTL
IVSREDDQFSYRMLINAPANTFAEKEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRTGERADIDIIGAICPPOALLTLIFTVVIIPLLMVLGRPAPINLVPIVFAVLIGLLL
CSALALMTSGFTRNAERAQMTSMPVFMLAMGGLGSIRFVFGDSIVADILAYTPFRAIS
DLVQIGWAGATFADSVGGVEAANFAGIFQDMLIPLGILAAWTAAAVWAANKYMRWDSY
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ytrvslgaipvvllsayflgivanagtinpsfvwilgfsvillivtvlvysygpsins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATVFPVGI PLLLFLIGNGGAAESANSFDYFVMYTLLFVQFYTVLSMATTRDERVLKR
                                                                                                                                               IIGR01184:ntrCD: nitrate transport ATP-binding subunits C
                                                                                                                                                                                                    TIGR01186:proV: glycine betaine/L-proline transport ATP binding subunit TIGR01187:potA: spermidine/putrescine ABC transporter
                                                                                                                                                                                                                                                                                                                 TICR01188:ďrrA: daunorubicin resistance ABC transporter
ATP-binding subunit
TICR01189:ccmA: heme exporter protein CcmA"
                                         IIGR00968:3a0106801: sulfate transport system permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i879. .6138

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/codon start=1
/transI table=11
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                                                                                             MIGR01166:cbiO: cobalt transport protein ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="ABC-type transporter, permease components"
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/db xref="G1:21323714"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="PF00072:Response regulator receiver domain
PF00196:Bacterial regulatory proteins, luxR family'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB98342.1"
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                 (IISP) Family protein
                                                                                                                                                                                                                                                                                            ATP-binding subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4003. .4836
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/transl_table=
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Query Match Best Local S Matches 873		61 AACCCGAATGCGTATTTGGACGCGTTTGTTGGCGGCGCGCGC	Db 128488 AACCCGAATGCGTATTTGGTGTTTGTGTTTATCGGCGGCGTGGGCGCGCGC	Db 128428 daCaccedaAceardeArririceCcecresceGerriceCceGeraceAccrearcrescres 128369 Qy 181 CTGGTGGGTTTCGGCGCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCCC 240	Db 128368 CTGGTGGTTTCGGCAGCAGCAGCAGCCCGCCCCAAGGTGTGGCC 128309 Qy 241 TGGATCAACGTCGTGGCAGAGTTGTAGACGCATTGGCCATTGGCCATTGAATGATGTTGTG 300	Db 128308 TGGATCAACGTGGGGGGGGTTTGTGGTGCGCGCTTTGGGCCATCAACTGATGTTGTGTG 128249 Qy 301 GGTTAGTTTTCGCGGGTTTTTGGAAATCGTGGCCCAAATGTTGGCGGCGTCG 360	Db 128248 GGTTAGTTTTCGCGGGTTTTTGGAATCGTGGCTTTCGCCTTCGCCTCAATGTTGATGCCGGCGTCG 128189 Qy 361 TGGGAAATCTCATCGATCGCCTCCAACTCGGGGGAAAAACTCCAAGTTGTTGAGTGAA 420	Db 128188 TGGGAATCTCTCTGTCTCTCTCTCTGTTGTTGTTGTTGTTGATGA 128129 Qy 421 TCAAGGCTGTTGTCCCAGCTGCTCAACTGAAGGCCCAATGCACTGTTGTCACTA 480	Db 128128 TCAAGGCTGTTGTTGTTGTTGTGTGTGTGTGTGTGTGTGT	Db 128068 TCGCGCGTACTCTCCTTGCGCGCAGCCCCATGCAGCGCCTGCGCAAGTGAC 128009 Qy 541 TGCCCGGGTTCCTGGGCGATGTCATTGAGCTTGCGGACCATATGATATTGTTCACGTTC 600	128008	Db 127948 AdvanceCricalcadeachtriaceCricacideachteccricachartrecarder 220
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HARUHIKO YOKOI,NAOKO TATEISHI,AKIHIRO SENOO,MASATO IKEDA,AKIO
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                                                    Patent: JP 2002191370-A 3454 09-JUL-2002;
KYOWA HAKKO KOGYO CO LTD
OS COTYNEDACCETIUM Glutamicum
PN 4D 2002191370-A/3454
PD 09-JUL-2002
PF 15-DEC-2000 JP 2000405096
PI SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,
                                                                                                                                                                                                                                                                                                                                           04, C12P13/08,
C12P19/00, C12P19/34, C12P21/02, C12Q1/37, C12Q1/68, G01N33/53,
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Location/Qualifiers
Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoo, A., Ikeda, M. and Ozaki, A. Novel polynucleotide
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               Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                         Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K., Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
Novel polynucleotides
Patent: EP 1108790-A 3454 20-UN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
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ASGKALYVGISSYGPELTARAAEFWAREGCFLLIHQPSYSIINRWVEEPGDDGSRLLQ
SAANNGLGVIAFSPLAGGLLTUYKLDGIPEGSRASQGKSLSEGMLNVNNIDMVRKLND
IAQERGOSLAGWALAWVLREGGSYGADTVTSALIGASSVEQLDNSLDSLNNLEFSDAE
LEAIDEIGHDAGINIWAKATDSKTREN"
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LSTQRSIIHRAFDRGVTHFDLANNYGPPAGSAETNFGRILREDLKSHRDELIISSKAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1023 AATCTCATCGATCGCCTCCAACTCGGCGTCAGAAACTCCAAGTTGTTGAGTGAATCAAG 964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zelder,O., Pompejus,M., Schroeder,H., Kroeger,B., Klopprogge,C.
Haberhauer,G.
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Corynabacterium glutamicum
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genes encoding for membrane synthesis and membrane transport
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Pred. No. 1.6e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="unnamed protein product; RXA07013"
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/mol_type="unassigned DNA"
/db_xref="taxon:1718"
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                                                                                                                                                                                                            Sequence 211 from Patent WO03040292. AX813971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent: WO 03040292-A 211 15-MAY-2003;
BASF AKTIENGESELLSCHAFT (DE)
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                                       CGCCTCCGCTGTGAGCTCTGGACCGTAG 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transT_table=11
/protein_id="CAEB1915.1"
/db_xref="G1:38636297"
                                                                   87 CGCCTCCGCTGTGAGCTCTGGACCGTAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .1083
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Conservative 0;
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LLLAFGFSLATWARDRGEVEMPVVGWGLLGRIPGSVLGTWAVVAMFVAGLKIVUATAV
TLGTISLVGWSPGHGRRNSFLAGASGGFLGTTTAIGGPPLALIMRSMSPERVRGTLS
VCFVIGSALSTALITGAGALGWMFILQAALVYAPAVIAGYFLSGVVNKHLNRRLIFLGS
VIISIGSGMVITQAAGIP"
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AMFHTIRQOPDAGSVWGQAREVVARCEQKFPDVADYLEBALDELLAFTNAPKSVWTKV
WSNNPTERLNREIRRRIDVVGIFPNRDAVVRLVGAVLABGHDDWIQOKRYWSLTSLEQ
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SNAQGCPGANGLPQNIVPIYRNPTFSRADREILNWASGAITTSELQELIEEAKELGRS
RELVKEFVASKGG"
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FTQQISYETSGDNLSATLTLTPGSITGATADAADAALATELNDTTTIDLGELPTSITG
SGWTYTFEGQVRGSGVSALSIKQAA"
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vcgadyatvsgdrvytrngyrhrdfdtrvgtidvavpklrtgsffpdmllbrrtraer
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PYLYVSCDALTMKVREGGRVVKTSVLLATGVNAEGYRELLGMQVATAESVASWTGFPR
             VHGITAGGAGETNQTAELIAGFEDMRAADVAKELYGLPKEQRDVAGGELDDERLADIL
QELSEDRQAELIETLDIERAADVLERMDPDADLIGELPEDRAGYLLELMDPEESAP
VRRIMGFRUDTYGALMTPEPLIMDPSTTVAEALAMARNPDLPTSLASIVEVVRPPTAT
PTGKTLGVHLIQKLIKEPPSSLVGGILDPDLPPLPPLYANDSQETAARFPATYLVCGPVL
DENGHLIGAVAVDDLLDHMLPEDWRDAGIRPGVKEETLG"
                                                                                                                                                                                                                                       /product="conserved hypothetical protein"
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/b xref="d1:2493024"
/b xref="d1:2493024"
/b xref="d1:2493024"
/cramslation="MAMQATGSGGNNRAELGLKKRPEGMPUGSFQTYEEAQRAVDMLS
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SSLLTGLVMGVVFGVVLAAVPFWASRGKRDFTSATQIVAGRYDILCRPDRAREARDMI
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ENLYIAVDPDYLGHNVISELYKTVLGNRGRFAVIRHEDNLIADPFDFLNEGTSDLVIG
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/HTDDPELEQLHGRAVEIADVELEQTRTRDWVISRVALIGERPKFGRRPTLYIAPWSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="CE1187, similar to AE007262-3|AAK65408.1| percent
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identity: 60 in 155 aa"
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protein id="BAC17997.1"
/db_xref="GI:23493026"
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protein_id="BAC17996.1"
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/protein_id="BAC17998.1"
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complement(11439. .15143)
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/protein_id="BAC17999.1"
/db_xref="GI:23493028"
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transl_table=11
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/transl_table=11
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'note="CE1188"
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186844 AGCAGGCCCTGCGCCAACGGGAAAGGCGATCACCCCCAGTCCGTTGTTCGCAGCGGCC 186785
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                                                                                                                                                                                                                                                                                                                                 436 AGCTGCTCAACTGACGAAGCACCAATCAATGCACTGGTCACGGTATCCGCGCCGTACTCT
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                                                                                                          GTTTTGGAATCGGTGGCCTTCGCCCAAATGTTGATGCCGGCGTCGTGGGAAATCTCATCG
                                                                                                                                                                                                                       376 ATCGCCTCCAACTCGGCGTCAGAAACTCCAAGTTGTTGAGTGAATCAAGGCTGTTGTCC
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                                                     Gaps
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Corynebacterium glutamicum
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
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/note="unnamed protein product; RXA01394"
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/mol_type="unassigned DNA"
/db_xref="taxon:1718"
                                                     0; Mismatches 143;
Score 329.2; DB
Pred. No. 3.2e-63
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BASF AKTIENGESELLSCHAFT (DE)
Location/Qualifiers
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Sequence 53 from Patent WO0100843.
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/protein_id="CAC25127.1"
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LIDREVFIGGVGAQYGDTGRWIFRAAGAFAASLIMFPLVGFGAAALSRPLSSPKVWRWIN
VVVAVVWTALAIKLMLMG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gunji,Y. and Yasueda,H.
Method for producing 1-lysine or 1-arginine by using methanol assimilating bacterium
Patent: EP 1266966.A 7 18-DEC-2002;
Ajinomoto Co., Inc. (JP)
Location/Qualifiers
                                                               Gaps
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                           Length 822;
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                                                                 Indels
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                             37.3%; Score 326; DB 6; I
100.0%; Pred. No. 2.2e-62;
iive 0; Mismatches 0;
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1. .711
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Best Local Similarity 100.
Matches 306; Conservative
                                                                     Conservative
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                                                  Similarity
                                                                     326;
                                Query Match
Best Local Si
Matches 326
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ORIGIN
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ETTEPTTGGVGAQAQCTGTWHIFAAGAFAASLIMFPLVGFGAALGSRPLSSPKWRWINVVV
AVVMTALAIKLMLMG"
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Corynebacterium glutamicum genes encoding metabolic pathway
                                                                                                                                                                                                                                                                                                                 AACCCGAATGCGTATTTGGACGCGTTTGTGTTTATCGGCGGCGTCGGCGCGCAATACGGC
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                                                                                                                                                                  Length 822;
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/101 802
/note="unnamed protein product; RXA01394"
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                                                                                                                                                                    37.3%; Score 326; DB 6; I
100.0%; Pred. No. 2.2e-62;
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/db_xref="REMTREMBL:CAC88508"
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BASF AKTIENGESELLSCHAFT (DE)
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Sequence 51 from Patent WO0166573.
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Corynebacterium glutamicum
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AX244059.1 GI:15859123
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Best Local S
Matches 326
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AX244059
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0y 181 CTGGTGGGTTTCGGCGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGC 240 Db 587 CTGGTGGGTTTCGGCGCAGCAGTTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGC 646 Oy 241 TGGATCAACGTCGTCGTGGTGATTGTTGATGATGATCAACTCAAGTTGATG 300 Db 647 TGGATCAACGTCGTCGGCAGTTGTGATGATGATGATGATGATGATGATGATGATGATG	RESULT 14 AX123539 LOCID LOCID AX123539 AX123539 AX123539 AX123539 AX123539 AX123539 AX123539 AX123539 GI:14041027 KEWORDS COTYnebacterium glutamicum ORGANISM COTYnebacterium glutamicum ORGANISM COTYnebacterium glutamicum ORGANISM COTYnebacterium glutamicum AATIONALE ACTIONACETAISS	Corynebacterineae; Corynebacteriaceae; Corynebacterium. REFERENCE 1 AUTHORS Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K., Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A. TITLE Novel polynucleotides JOURNAL Patent: BP 1108790-A 3455 20-UUN-2001; KYOWA HAKKO KOGYO CO., LTD. (JP) FEATURES 1. 708 1. 708 / Anganism="Corynebacterium glutamicum" // Ab xref="umasigned DNA"	ORIGIN Query Match 34.7%; Score 303; DB 6; Length 708; Best Local Similarity 100.0%; Pred. No. 3.1e-57; Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATGGTGTGACCTGGTTG 60 Db 406 GTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTG 60		Qy 241 TGGATCAACGTCGTGGTGATGATGATGATGACGATTGGCCATCAAACTGATGTTGATG 300 bb 646 TGGATCAACGTCGTGGGCAGTTGTGATGACGCATTGGCCATCAAACTGATGTTGATG 705 Qy 301 GGT 303 11 Db 706 GGT 708	RESULT 15 BD165656 LOCUS LOCUS DEFINITION Novel polymucleotide. ACCESSION BD165656. VERSION BD165656.1 GI:27871468 KEYWORDS JP 2002191370-A/3455.
406 GTCGATAAGCAGCGGTTTGGGTAAAGCCCCATGTTGATGGCAATCGTGCTGACCTGGTTG 61 AACCCGAATGCGTATTTGGACGCGTTTGTTTTTTTTACGGGGGGTCGGCGCGCAATACGGC 466 AACCCGAATGCGTATTTGGACGCTTTGTGTTTATCGGCGGGCG	DB SB6 CTGGTGGGTTTCGGCGGGGGGTTTGTCACCCCCTGTCCACCCCAAGGTGTGGCGC 845 QY 241 TGGATCAACGTCGTGGGGGGTTGTGATGGCCATTGGCCATCAAACTGATGTTGATG 300 C46 [AIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		AUTHORS Gunji, Y. and Yasueda, H. TITLE Method for producing 1-lysine or 1-arginine by using methanol assimilating bacterium JOURNAL Patent: EP 1266966-A 9 18-DEC-2002; Rjinomoto Co., Inc. (JP) FRATURES 1. 772 Source /organism="Corynebacterium glutamicum" /mol type="unassigned DNA"	/db xref="taxon:1718" 1. 375 /once="unnamed protein product" /codon start=1 /codon start=1 /protein id="Cab67812.1" /db xref="G1:2855016." /db xref="G1:2855016." /db xref="G1:2855016." /translation="MYNEMEL:CAD67812." /translation="MYNEMEL:CAD67812." /translation="MYNEMERTGELIGABLILSIGPONULVIKQGIKREGLIAVILIV /translation="MYNEMERTGELIGABLILGABLILSIGPONULVIKQGIKREGLIAVILIV /translation="MYNEMERTGELIGABLILGABLILGABLINGABLIAVILIV /translation="MYNEMERTGELIGABLILGABLILGABLINGABLINGABLIAVILIV /IRETERPTVPDDTPLGVFGGGH" ORIGIN	Query Match 34.9%; Score 304.4; DB 6; Length 712; Best Local Similarity 99.7%; Pred. No. 1.5e-57; Matches 305; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 GTCGATAAGCAGCGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGTTG 60 Db 407 GTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTG 60	Qy 61 AACCCGAATGCGTATTTGGACGCGTTTATCGCGGGGGCGCGGCGCATACGC 120 Db 467 AACCCGAATGCGTATTTGGACGCGTTTGTTTATCGGCGGCGCGTCGGCGCGAATACGGC 526 Qy 121 GACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCCGC 180 Db 527 GACACCGGACGGTGGATTTTCGCCGCTGGCGCTTCGCGGCAAGCCTGATCCCG 586

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A LOBARDA LO. OCHIAI, R. Ando, S., Hayashi, M., Ochiai, K.,
Yokoi, H., Tateishi, N., Senco, A., Ikeda, M. and Ozaki, A.
Yokoi, H., Tateishi, N., Senco, A., Ikeda, M. and Ozaki, A.
Novel polymuclectide

I. Patent: JP 2002191370-A 3455 09-JUL-2002;
KYOWA HAKKO KOGYO CO LTD
OS COTYNEBACCETIUM Glutamicum
PN JP 2002191370-A/3455
PD 09-JUL-2002
PF 15-DEC-2000 JP 2000405096
PI SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,
PI KEIKO OCHIAI,
PI HARUHIKO YOKOI, NAOKO TATEISHI, AKIHIRO SENOO, MASATO IKEDA, AKIO
PI OZAKI

PC CIZNIS/09, CIZNIS/09, COYKIA/34, COTKIE/12, COTKIE/40, CIZMI/00, PC
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PC 04,C12P13/08,
PC C12P13/00,C12P19/34,C12P21/02,C12Q1/37,C12Q1/68,G01N33/53, PC
G01N33/566,
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| organism='Corynebacterium glutamicum'.
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Matches 303; Conservative 0; Mismatches 0;
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/organism="unidentified"
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AUTHORS
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	AAT96816 Aat96816 DNA encod	ADB66196 ADB66196 DNA fragm	AAH68528 C glutami	AAH68419 C glutami		AAF71779 Corynebac	AAS96098 C. glutam	ACC80941 Acc80941 LysE prot	ACC80942 ACC80942 LYBE24 pr	AAH68420 C glutami	ACA29651 Aca29651 Prokaryot	AAH45375 C. thermo	ACA25567 Aca25567 Prokaryot	ACA26520 Aca26520 Prokaryot	ACA24017 Aca24017 Prokaryot	ACA32095 Aca32095 Prokaryot	ACA19150 Aca19150 Prokaryot	ACA45509 Aca45509 Prokaryot	ACA51519 Aca51519 Prokaryot	ACA50894 Aca50894 Prokaryot	AAQ55755 Escherich	
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The present invention relates to a method for producing L-arginine in a microorganism (e.g. coryneform bacteria) that has L-arginine producing ability and has been modified for enhanced expression of the 198E gene. The microorganism is also modified so that an arginine repressor (argR) does not function normally. The method of the invention is useful for the enhanced production of L-arginine which is useful in liver function promoting agents, amino acid infusion and comprehensive amino acid pharmaceuticals. The present sequence represents a DNA fragment containing Corynebacterium alutamicum Ly8G and Ly8E genes. Note: The present sequence is given as SEQ ID No:24 in the Sequence Listing but is referred to as SEQ ID No:25 in the rest of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AACCCGAATGCGTATTTGGACGCGTTTGTGTTTTATCGGCGGCGTCGGCGCGCAATACGGC 120
A microorganism comprising enhanced expression of the lysE gene is useful for enhanced production of L-arginine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GICGAIRAGCAGCGGGTIIGGGIRAAGCCCCAIGIIGAIGGCAAICGIGCIGACCIGGIIG 60
                                                                                                                                                                                                                                                                                                               L-arginine production; coryneform bacteria; lysE; arginine repressor; argR; liver function promoting agent; amino acid infusion; amino acid pharmaceutical; LysG; ds.
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                                                                                                                                                                                                                                                                                DNA fragment containing C. glutamicum Ly8G and LySE genes
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                                                                         2261 TCAGCCGCCTCCGCTGTGAGCTCTGGACCGTAG 2293
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                                                          841 TCAGCCGCCTCCGCTGTGAGCTCTGGACCGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1025. .1726
                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-2002; 2002US-00196232
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                                                                                                                                                                                 ADB66196 standard; DNA; 2374
                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum.
                                                                                                                                                                                                                                                    04-DEC-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamaguchi M, Ito H,
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                       This DNA, isolated from Corynebacterium glutamicum, contains the LysG, LysE and ORF3 genes. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene. NB. This sequence has been created from the information given in table 2 of the
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100.0%; Pred. No. 4.9e-246;
tive 0; Mismatches 0; Indels 0,
                                                                                                                                                                                                                                                          Sequence 2374 BP; 526 A; 640 C; 648 G; 560 T; 0 U; 0 Other;
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Matches 873; Conservative
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Ochiai K,

H, Ando S, Hayashi M, Ikeda M, Ozaki A;

Mizoguchi H, Senoh A, Ik

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, messuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, coryneform bacterium, saccharides and organic acide from particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                           mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 349980 BP; 80727 A; 91049 C; 97618 G; 80586 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 7063; 246pp + Sequence Listing; English.
                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO KK
              18-DEC-2000; 2000EP-00127688
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Matches 873; Conservative
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07-APR-2000;
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Tateishi N,
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          CTGGTGGGTTTCGGCGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGC
                                       241 TGGATCAACGTCGTCGTGGCAGTTGTGATGACCGCATTGGCCATCAACTGATGTTGATG
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Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

organic acid synthesis; ds. Corynebacterium glutamicum.

EP1108790-A2

20-JUN-2001

glutamicum coding sequence fragment SEQ ID NO: 7063

(first entry)

26-SEP-2001

AAH68528

BP

AAH68528 standard; DNA; 349980

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                                                                                                                                                               127888 AGATATTTGTCCGTGAGCAGGCCCTGCGCAAGTGGTGAGAAAGCAATGACGCCAAGACCA 127829
                                                                                                                                                                                                                                                                       128068 TCCGCGCCGTACTCTCCTTGCTCGCGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGAC 128009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, mesauring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium.
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                                             TGCCCGCGTTCCTGGGCGATGTCATTGAGCTTGCGGACCATATCAATATGTTCACGTTC
                                                                              AACATGCCCTCAGACAGGGACTTACCCTGGCGCGGGGAACCCTCTGGAATTCCATCG
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                                                                                                                                                                                                                                                                                                                    127708 TCAGCCGCTCCGCTGTGAGCTCTGGACCGTAG 127676
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Ikeda M, Ozaki A;
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07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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                                                                                                                                                                                                                                                                                                                                                                                                 AAH68419 standard; DNA; 627
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Senoh A,
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acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the Buropean Patent Office
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0
                                                                                                                                                                                                                                                                                                                                                                     Length 627;
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Pred. No. 1.5e-156;
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ilarity 100.0%; Pred. No. 1.5
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    993 AGCACCAATCAATGCACTGGTCACGGTAATCCGGCGCCGTACTCTTTTGCTCGCGCAGC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum, metabolic pathway protein, MP protein, fine chemical production, microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unaaturated fatty acid; unaaturated fatty acid; carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum MP protein nucleotide sequence SEQ ID NO:53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGCGGACCATATCAATATTGTTCACGTTCAACATGCCCTCAGACAGGGACTTACCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGTCATCGCCCGGTTCCTCCACCCAACGATTAATGATGGATAGCTTGGCTGGATGAATC
                                                       ACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGCGTTCCTGGGCGATGTCATTGAGC
                                                                                   631 CTGGCGCGCGCAACCCTCTGGAATTCCATCGAGATATTTGTCCGTGAGCAGGCCCTGCGCA
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9908-01031415.
9908-01031418.
9908-01031419.
9908-01031420.
9908-01031420.
9908-01031428.
9908-01031434.
9908-01031434.
9908-01031435.
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08-70L-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacteium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation.
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Local Similarity 98.8%; Pred. No. 2.7e-108;
les 418; Conservative 0; Mismatches 3; Indels 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 1107-1108; 1119pp; English.
                                                                                                         99US-0141031P.
99DE-01031454.
99DE-01031478.
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99DE-01032124.
99DE-01032125.
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99DE-01032229.
99DE-0103230.
99DE-01032927.
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99DE-01040765.
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99DE-01040830.
99DE-01040831.
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99DE-01041378.
99DE-01041379.
99DE-01041395.
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99DE-01042078.
99DE-01042079.
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99DE-01032212.
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99DE-01033006
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99DE-01032180
                                                             2000WO-IB000926
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09-7UL-1999;
14-7UL-1999;
14-7UL-1999;
14-7UL-1999;
27-AUG-1999;
                                                             23-JUN-2000;
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27-AUG-1999;
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31-AUG-1999

03-SEP-1999 03-SEP-1999

27-AUG-1999 27-AUG-1999

09-JUL-1 09-JUL-1 09-JUL-1

Query Match Best Local Si Matches 418

453 AGCACCAATCAATGCACTGGTCACGGTA--TCCGCGCCGTACTCTCCTTGCTCGCGCAGC 510

99DE-01031478. 99DE-01031510. 99DE-01031541.

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241 IGGATCAACGTCGTCGTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATG 300
                                                                                                                         AACCCGAATGCGTATTTGGACGCGTTTGTGTTTATCGGCGGCGTCGGCGCCGCAATACGGC
           GACACCGGACGGTGGATTTTCGCCGCTGGCGTTCGCGGCAAGCCTGATCTGGTTCCCG
                                                                           181 CTGGTGGGTTTCGGCGCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCCAAGGTGTGGCGC
                                                                                                                                                       301 GGTTAGTTTTCGCGGGTTTTGGAATC 326
                                                                                                                                                                         797 GGTTAGTTTTCGCGGGTTTTTGGAATC 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and
                                                                                                                                                                                                                                                                                                                                                                                                                        Haberhauer G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 167 A; 192 C; 246 G; 217 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.3%; Score 326; DB 4; I 100.0%; Pred. No. 2.5e-85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. no. -
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                                                                                                                                                                                                                                                                                                                                                                                                                         Schroeder H,
                                                                      99DE-01032130
99DE-01032186.
99DE-01032206.
99DE-01032227.
99DE-01032228.
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99DE-01041394.
99DE-01042076.
99DE-01042077.
99DE-01042079.
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99DE-01042088.
99DE-01042095.
99DE-01042124.
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99DE-01032125.
99DE-01032126.
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99DE-01032928.
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99DE-01040764.
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                        99DE-01031632
99DE-01031634
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Matches 326, Conservative
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                                                                                                                                                                                                                                                                                                       03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
      08-JUL-1999;

08-JUL-1999;

08-JUL-1999;

08-JUL-1999;

09-JUL-1999;

09-JUL-1999;

09-JUL-1999;

09-JUL-1999;

09-JUL-1999;

09-JUL-1999;

14-JUL-1999;

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14-JUL-1999;

14-JUL-1999;

14-JUL-1999;

14-JUL-1999;

14-JUL-1999;

14-JUL-1999;
                                                                                                                                                                                               12-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
31-AUG-1999;
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The present invention relates to the isolation of novel Corynebacterium glutamicum genes encoding metabolic pathway (MP) proteins (AAU71863-AAU71922). The metabolic pathway proteins of the invention include enzymes involved in the lysine and methionine biosynthetic pathways. The polymuclectide sequences of the invention can be used for the large-scale production and/or modulation of expression of fine chemicals such as lysine and methionine. The sequences of the invention may be used to identify C. glutamicum and related organisms e.g. C. diphtheriae in a subject to detect diphtheria. AAS96073-AAS96132 represent C. glutamicum genes encoding the novel metabolic pathway proteins of the invention
                                                                        Metabolic pathway protein; MP; lysine biosynthesis pathway;
methionine biosynthesis pathway; large-scale production of fine chemical;
Corynebacterium diphtheriae; diphtheria; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding metabolic pathway proteins from Corynebacterium glutamicum, useful for producing methionine and lysine in Corynebacterim and Brevibacterium.
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    c. glutamicum gene #23 encoding metabolic pathway protein.

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23-JUN-2000; 2000US-00606740.
                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum.
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Lee H, Hwang B;
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1 GICGATAAGCAGCGGGGITIGGGTAAAGCCCCATGITGAIGGCAAICGIGCIGACCIGGITG

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bacterium when introduced into the bacterium. The method is used for encoding a protein which facilitates excretion of L-lysine, L-arginine or both of these L-amino acids to outside of a cell of a methanol assimilating bacterium when DNA of the method is introduced into the bacterium. The present sequence represents a lysk protein from the present sequence represents a lysk protein from the bacterium lactofermentum encoding sequence. (Updated on 27-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                         61 AACCCGAATGCGTATTTGGACGCGTTTGTGTTTTATCGGCGGCGTCGGCGCGCAATACGGC
                                                                                                                                                                                                                                                                                                          GACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCCG
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                                                                                                                                                              Length 711;
                                                                                                                              Sequence 711 BP; 135 A; 173 C; 222 G; 181 T; 0 U; 0 Other;
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                                                                                                                                                              Score 306; DB 8; I
Pred. No. 1.8e-79;
                                                                                                                                                    35.1%; Scc...
100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L-lysine; L-arginine; LysE24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUN-2001; 2001JP-00177075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-2002; 2002EP-00012539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACC80942 standard; DNA; 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
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                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gunji Y, Yasueda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-241171/24.
P-PSDB; ABR58214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTTAG 306
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                                                                                                                                                                              Similarity
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11-AUG-2003
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                                                                                                                                                                                             Matches 306;
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                                                                                                                                                               Query Match
                                                                                                                                                                                  Local
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CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to DNA encoding variants of protein with loop region and six hydrophobic helixes which facilitates excretion of L-lysine and/or L-arginine to outside of cell of a methanol assimilating
                                                                                                                                 120
                                                                                                                                                            180
                                                                                                                                                                                                                             9/9
                                                                                                                                                                                                                                                             240
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                                                                                                  GICGALAAGCAGCGGGTITIGGGTAAAGCCCCATGTTGATGGCAATCGTGCTGACCTGGTTG 556
                                                                                                                                                                                                                                                                                                                          TGGATCAACGTCGTCGTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATG 300
                                                                     09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel DNA encoding variant of LysE protein from a coryneform bacterium, when introduced into methanol assimilating bacterium, facilitates excretion of L-lysine and/or L-arginine to outside of a cell.
                                                                                                                                                                                                 GACACCGGACGGTGTTTTCGCCGCTGGCGCTTCGCGGCAAGCCTGATCTGGTTCCCG
                                                                                                                                                                                                                   617 GACACCGGACGGTGGATTTTCGCCGCTGGCGCTTCGCGGCAAGCCTGATCTGGTTCCCG
                                                                                                                                                                                                                                                             CTGGTGGGTTTTCGGCGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGC
                                                                                                                                                                                                                                                                                    CTGGTGGGTTTCGGCGCAGCAGCATGTCACGCCCCGCTGTCCAGCCCCAAAGGTGTGCCC
                                                                                                                                                                                                                                                                                                                                              1 GICGAIAAGCAGCGGGITIIGGGIAAAGCCCAIGIIGAIGGCAAICGIGCIGACCIGGITG
                                      Gaps
                                      ;
0
      Length 822;
   37.3%; Score 326; DB 4; Length 82.
100.0%; Pred. No. 2.5e-85;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .711
/*tag= a
/product= "lysE protein"
                                                                                                                                                                                                                                                                                                                                                                                          GGTTAGTTTTCGCGGGTTTTGGAATC 326
                                                                                                                                                                                                                                                                                                                                                                                                                      GGTTAGTTTTCGCGGGTTTTGGAATC 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 17-18; 23pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-lysine; L-arginine; LysE; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysE protein encoding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACC80941 standard; DNA; 711
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 Ouery Match 5/100.

Best Local Similarity 100.
Matches 326; Conservative
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11-AUG-2003
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18-DEC-2002

Gunji Y,

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                                                                                                The present invention relates to DNA encoding variants of protein with loop region and six hydrophobic helixes which facilitetes excretion of Lusine and/or Lusquine to outside of cell of a methanol assimilating bacterium when introduced into the bacterium. The methan is used for encoding a protein which facilitates excretion of Lulyshie, Lusquinie or both of these Lumino acids to outside of a cell of a methanol assimilating bacterium when DNA of the method is introduced into the bacterium. The present sequence represents a lysE24 protein from the struktacterium lactofermentum encoding sequence. (Updated on 27-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                              9
         Novel DNA encoding variant of LySE protein from a coryneform bacterium, when introduced into methanol assimilating bacterium, facilitates excretion of L-lysine and/or L-arginine to outside of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GTCGATAAGCAGCGGGTTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                         61 AACCCGAATGCGTATTTGGACGCGTTTGTGTTTATCGGCGCGTCGGCGCGCAATACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACACCGGACGGTGGATTTTTCGCCGCTTCGCGGCAAGCCTGATCTGGTTCCCCG
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                                                                                                                                                                                                                                                                                                Score 304.4; DB 8; Length 712;
Pred. No. 5.3e-79;
                                                                                                                                                                                                                                                                     Sequence 712 BP; 133 A; 173 C; 224 G; 182 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C glutamicum coding sequence fragment SEQ ID NO: 3455.
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                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                        Example 1; Page 19-20; 23pp; English
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07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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                                                                                                                                                                                                                                                                                                   34.9%;
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                                                                                                                                                                                                                                                                                                                                   Matches 305; Conservative
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                                                                                                                                                                                                                                                                                                                     Local Similarity
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Best Local S
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologum of a gene derived from coryneform bacterium, coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466 AACCCGAAIGCGTATTIGGACGCGTTTGTGTTTATCGGCGGCGTCGGCGCGCAATACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 IGGATCAACGICGICGIGGCAGIIGIGAIGACCGCAIIGGCCCAICAAACIGAIGIIGAIG
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                                           Yokoi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 34.7%; Score 303; DB 5; Length 708; al Similarity 100.0%; Pred. No. 1.4e-78; 303; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                            Claim 1; SEQ ID NO 3455; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 708 BP; 134 A; 173 C; 221 G; 180 T; 0 U; 0 Other;
                                           Ochiai K,
                                           Nakagawa S, Mizoguchi H, Ando S, Hayashi M,
Tateishi N, Sench A, Ikeda M, Ozaki A;
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ACA29651 standard; DNA; 1095 BP.
           (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium diphtheriae.
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Best Local Similarity
                                                                                                  WPI; 2001-376931/40.
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                                                                                                                       P-PSDB; AAG93201
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TTGTCCAGCTGCTCAACTGACGAAGCACCAATCAATGCACTGGTCACGGTATCCGCGCCG
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                                                                                                                                                                             914 TAATCGCCTTGTTCCCGCAGCACCCACGCAATAGCCAGCTGTGCCAACGTTTGGCCACGT
                                                                                                                                                                                                                                                                     550 ICCIGGGCGAIGICALIGAGCIIGCGGACCAIAICAAIAIIGIICACGIICAACAIGCCC
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                                                                                                                                  TACTCTCCTTGCTCGCGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGCGT
                                                                                                                                                                                                                                                                                                                                                                                                        TCAGACAGGGACTTACCCTGGCTGGCGCGGGAACCCTCTGGAATTCCATCGAGATATTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A heat-resistant lysin biosynthetic system enzyme gene of a high temperature-resistant coryneform microbe.
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aspartate-semialdehyde dehydrogenase; lysE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 22-24; 27pp; Japanese.
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(1) a vector comprising a promoter operably linked to the nucleic acid conformation of the nucleic acid conformation of the vector; (3) and isolated proliferation is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding composition or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that inhibits cellular proliferation, or that inhibits cellular proliferation of an pathway in which a proliferation-required gene or the biological pathway capables in which the test compound that inhibits proliferation of an open which the test compound that inhibits proliferation of an compound a activity (11) a culture comprising strains in which the gene product is overexpressed or underexpressed, (12) determining the extent compound sactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed, (12) determining the extent compound capating in which the strains is present in a culture or collection of confound an organism. The antisense nucleic acids are useful for the collarity collection of an organism. The antisense nucleic acids are incomposed for a compound for an organism of the prights proteins or screening for homologous nucleic acids are incomposed.
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Xu HH;
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for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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Forsyth RA,
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Pred. No. 5.5e-64;
0; Mismatches 194;
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Yamamoto R,
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Carr GJ,
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2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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Best Local Similarity 65.6
Matches 370; Conservative
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Trawick JD,
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                                   WO200277183-A2.
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08-FEB-2002;
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polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding cantisense nucleic acid; (4) an antibody capable of specifically binding compound the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that inhibits biological pathway cequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acres; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the axtent of owlich each of the strains is present in a culture or collection of the which each of the strains is present in a culture or collection of the compound of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation to isolate andidate molecules for rational cultification in cells other than S. tryphimurium, required for proliferation in cells other than S. arreus, S. tryphimurium, control format directly from WiPO at compound of the target of electronic format directly from WiPO at
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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
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                                                                                                                                                                                                                                           189
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                                                                                                                                                                       GCGTATTTGGACGCGTTTGTGTTTTATCGGCGGCGTCGGCGCGCAATACGGCGACACCCGGA
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Xu HH;
                                                                                                    CAGCGGGTTTGGGTAAAGCCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAAT
                                                                   Gaps
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                                Length 1568;
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Yamamoto R, Forsyth RA,
                               Score 193.6; DB 4; Length:
Pred. No. 2.9e-46;
0; Mismatches 64; Indels
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Carr GJ,
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06-SEP-2001; 2001US-00948993.

25-CCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-03072851.

06-MAR-2002; 2002US-0362699P.
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                                  22.2%;
78.4%;
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                                                   al Similarity 78.4
232; Conservative
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug design; gene.
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Wall D,
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                                      Query Match
Best Local S
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                                                                                                                                                                                                                                                                                              391 GCGTCAGAAAACTCCAAGTTGTTGAGTGAATCAAGGCTGTTGTCCAGCTGCTCAACTGAC 450
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                                                                                                                                            42;
                                                                                               DB 7; Length 1041;
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                                          Sequence 1041 BP; 216 A; 316 C; 327 G; 182 T; 0 U; 0 Other;
                                                                                          Query Match 12.1%; Score 105.8; DB 7; Length Best Local Similarity 55.6%; Pred. No. 1.6e-20; Matches 293; Conservative 0; Mismatches 192; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           805 TGAATCAGAAGCGGGCAGCCCTCCTCCGCCATGAACTCAGCCGCCTC
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ftp.wipo.int/pub/published_pct_sequences
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24;

Mismatches 152; Indels

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The invention relates to an isolated nucleic acid comprising any one of the fell antisense sequences given in the specification where expression of the fell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid included are:

(1) a vector comprising a promoter operably linked to the nucleic acid contains a polypeptide whose expression is inhibited by the antisense nucleic acid; (3) a host cell containing the vector; (3) an isolated polypeptide cor its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding collypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operom required for proliferation or the activity of a gene in an operom required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene product that an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a product is overexpressed or underexpressed; (12) determining the extent convict acids activity; (11) a culture comprising strains in which the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits proliferation of strains; or (13) identifying the target of a compound that inhibits or servent confidention of an organism. The antisense nucleic acids are useful for the cellular proliferation to isolate candidate molecules acids required for collular proliferation to isolate candidate molecules acids required for cellular proliferation to isolate candidate molecules acids required for the cellular proliferation to isolate candidate molecules acids required for the cellular proliferation to isolate acids are usef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind JW;
Xu HH;
                                                                                                                                      Antisense; ds; prokaryotic essential gene; cell proliferation;
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Forsyth R
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Yamamoto R,
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                                                                                         Prokaryotic essential gene #8177.
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Carr GJ,
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06-SEP-2001; 2001US-00948993.

2-CCT-2010; 2001US-0342923P.

08-FEB-2002; 2002US-03072851.

06-MAR-2002; 2002US-0362699P.
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                                               (first entry)
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Trawick JD,
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P-PSDB; ABU22650.
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                                                                                                                                                                    drug design; gene
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                                               19-JUN-2003
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ACA26520;
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11.1%; Score 96.8; DB 7; Length 1107; 56.9%; Pred. No. 7.3e-18;

Best Local Similarity

Query Match

Sequence 1107 BP; 204 A; 360 C; 370 G; 173 T; 0 U; 0 Other;

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1092 GGACGGCTTTTCCCCACATTGATCCCGCCTTCGGTCGCATAGCGGTCGATCTCGGCGAT 1033
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Xu HH;
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Gaps
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for homologous nucleic acids required for cellular proliferation i
solate candidate molecules for rational drug discovery programs.
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Forsyth RA,
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Yamamoto R,
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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      Conservative
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Trawick JD,
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      Matches 232;
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Wall D,
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ACA24017/c
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the 6213 antieense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (11 a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense cull containing the vector; (3) an isolated cull surface acid; (2) a host cell containing the vector; (3) an isolated cull surface acid; (4) an antibody capable of specifically binding cullisense nucleic acid; (4) an antibody capable of specifically binding cullisense nucleic acid; (4) an antibody capable of specifically binding cullisense nucleic acid; (4) an antibody capable of specifically binding culliseration or the activity of agene in an operon required for the proliferation, or that inhibits cellular proliferation; (7) identifying a compound that inhibits proliferation of the gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits proliferation of an cranification of the strains agene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound that inhibits the compound's activity; (11) a culture comprising strains in which the gene compound that inhibits the compound's activity; (11) a culture comprising strains in which the gene compound is soverspressed or underexpressed, (12) determining the extent compound that inhibits the compound's activity; (11) a culture comprising strains in which the gene compound that inhibits the compound's activity; (11) a culture compound that inhibits the compound and or the strains is present in a culture or collection of conditiving proteins or screening for homologous nucleic acids required for proliferation in cells of the cellular proliferation in cells of the cellular profileration in cells of the cellular profileration in cells of the cellular profileration in cells of the cellular profileration in
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Search completed: March 15, 2004, 14:59:16 Job time : 357.983 secs

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Sequence 14, Appl
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Sequence 21, Appl
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Sequence 21, Appl
Sequence 2121, Appl
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Sequence 3864, Ap
Sequence 3864, Ap
Sequence 11, Appl
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                                                                          SCHWARE Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-AUG-1997
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                                                                                                                                                                                                                                                                                    CLASSIPTCATION: 435

PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/362,577

APPLICATION NUMBER: US 08/362,577

FILLING DATE: 27-MAR.1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547

REFERENCE/DOCKET NUMBER: 19036/32420

TELEPHONE: 312/474-6300

TELEPHONE: 312/474-6300
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STRAIN: Clinical Isolate EC-625
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Usana, Hirotsugu
APPLICANT: Bada, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
          Length 5541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
Score 71.6; DB 1; Length 55
Pred. No. 2.8e-11;
0; Mismatches 299; Indels
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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Patent No. 5770375
GENERAL INFORMATION:
                     Query Match
Best Local Similarity 49.4%;
Matches 337; Conservative
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US-08-920-827-20
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3088 GAACTITATICCCTTCACGATGCATCCGTGAATCTTGCGGAATGCCGTTGAGATATTTTC 3147
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                                                                                   383 CCAACTCGGCGTCAGAAACTCCAAGTTGTTGAGTGAATCAAGGCTGTTGTCCAGCTGCT
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APPLICANT: Matsuhisa, Akio
APPLICANT: Watsuhisa, Akio
APPLICANT: Ushara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disea
NUMBER OF SEQUENCES: 25
CORRESPONDENS: 25
CORRESPONDENS: ABDERSS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                           2927 cececece-recearcaarcaaraceacercacecarra----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAWE: Rin-Laures, Li-Heien
REGISTATION NUMBER: 33,547
REFRENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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APPLICANT: Ohno,
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US-08-362-577C-20
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                                                                   203 CATTGTCACGCCCGCTGTCCAGCCCCCAAGGTGTGGCCGCTGGATCAACGTCGTCGTGGCAG 262
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ohno, Teuneya
APPLICANT: Matenina, Akio
APPLICANT: Matenina, Hiroteugu
APPLICANT: Eda, Soji
TITEE OF INVENTION: Probe for Diagnosing Infectious Disease
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-PAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAWE: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Illinois
COUNTRY: United States of America
COUNTRY: 01066-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                               3313 TTTGCGTCCGCTCTGGCGAGTA 3334
                                                                                                                                            851 CCGCTGTGAGCTCTGGACCGTA 872
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STRAIN: Clinical Isolate EC-625
                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/08921177 Patent No. 5798211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 5541 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: Genomic DNA
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-921-177-20
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Pred. No. 2.8e-11;
0; Mismatches 299; Indels 46
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                                                                                                                                                                                 ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-625
                                                                                                                                                                                                                                                       Query Match 8.2%;
Best Local Similarity 49.4%;
Matches 337; Conservative
                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
                                                                    5541 base pairs
               TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
312/474-0448
                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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US-08-362-577C-20
TELEFAX:
                                                                  LENGTH:
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RESULT 5
US-08-920-828-20
US-08-920-828-20
Sequence 20, Application US/08920828
Patent No. 5853998
GENERAL INFORMATION:

APPLICANT: Ohno, Tsuneya

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                                                                  Probe for Diagnosing Infectious Disease
                                                                                                                                        & Borun
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                                                                                                                                        Gerstein, Murray &
South Wacker Drive
                                                                                                                                                                                                                                                          ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.2%; Score 71.6; DB 2;
49.4%; Pred. No. 2.8e-11;
ive 0; Mismatches 299;
                                                                                                                                                                                                                                                                                                                                                                                        CURENT APPLICATION DATA:
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
FILING DATE: 29-AMR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
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                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-625
                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                        Uehara, Hirotsugu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 49.4%;
Matsuhisa, Akio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 5541 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                        APPLICANT: Uchara, Hi
APPLICANT: Eda, Soji
IITLE OF INVENTION: P
                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                               STREET: b.c.
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US-08-920-828-20
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TELEX: 2
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Ruchige Arib And Amino acid sequences Relating to Pseudomonas.
TITLE OF INVENTION: AEROGINOSA POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PLING UNBER: 1089-102-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
SEQ ID NOS: 33142
SEG ID NOS: 33142
                                                                                               APPLICANT: Warc J. Rubenfield et al.

APPLICANT: Warc J. Rubenfield et al.

TITLE OF INVERTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.

TITLE OF INVERTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVERTION: 107166.136

CURRENT APPLICATION NUMBER: US 60/074,788

FRIOR PELING DATE: 1998-02-18

FRIOR PILING DATE: 1998-02-18

FRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 7643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 834;
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Pred. No. 9.7e-09;
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Sequence 7643, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
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Patent No. 6551795
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PALICATION NUMBER: US/09/252,991A
CURRENT PALICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PEPLICATION NUMBER: US 60/094,190
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7908
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     1088 GAACTTTATTCCCTTCACGATGCATCCGGGAATCCTTGCGGAATGCCGTTGAGATATTTTC 3147
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                                                                                                                                                            623 TACCCTGGCTGGC-
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US-09-252-991A-7908
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86 TIGICITITALCGGGGGGGTCGGCGCGAATACGGCGACACCGGACGGTGGATTTTCGCCG 145
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     Sequence 11, Application US/09894844
; Sequence 11, Application US/09894844
; Patent No. 668616
; GENERAL INFORMATION:
    APPLICANT: Behr, Marcel
    APPLICANT: Small, Peter
    APPLICANT: Schoolnik, Gary
    APPLICANT: Schoolnik, Gary
    TITLE OF INVENTION: Molecular Differences Between Species of
    TITLE OF INVENTION: Molecular Differences Between Species of
    TITLE OF INVENTION: Molecular Differences Between Species of
    TITLE OF INVENTION: Molecular Differences Between Species of
    TITLE OF INVENTION: Wolchel A.
    TITLE OF INVENTION: WORBER: US/09/894,844

CURRENT FILING DATE: 1999-06-27
; PRIOR FILING DATE: 1999-06-25
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ION NOS: 137
SOSTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SIQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 597;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPHTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Best Local Similarity 53.1%; Pred. No. 2.3e-07;
Matches 145; Conservative 0; Mismatches 125;
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California
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US-08-390-878-17/c
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JS-09-894-844-11
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LENGTH: 597
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APPLICANT: GATY Breton et. al

TITLE OF INVENTION:

NULLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PUEDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT PALICATION NUMBER: US/09/489,039A

CURRENT PILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
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339 IGGCGGCACTGGCGGTCACCCTGCTCAACCCCCACGTCTATCTCGATACCGTACTTCTGA 398
                                                                                                   155 TCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGCGCAGCAGCATTGTCACGCC 214
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                                                   TCGGCGGCGCGCGCGCAATACGGCGACCACCGGACGGTGGATTTTCGCCGCTGGCGCGT
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Pred. No. 1.7e-08;
0; Mismatches 178; Indels 21.
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US-09-489-039A-5370/c
. Sequence 5370, Application US/09489039A
, Patent No. 6610836
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Local Similarity 51.2%;
hes 209; Conservative (
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RESULT 10

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RESULT 14
US-09-252-991A-7571/c
; Sequence 7571, Application US/09252991A
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OTHER INFORMATION: H37Rv
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APPLICANT: FLEISCHMAN, Robert D.
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US-09-103-840A-1
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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Pred. No. 1.1e-06;
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APPLICATION NUMBER: US/08/390,878
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ORGANISM: Mycobacterium tuberculosis
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Patent No. 6294328
                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 1537.
TELECOMMUNICATION INFORMATION:
TELEPRONE: 415/543/5603
TELEPRONE: 415/543/56043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15239 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                 NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
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Best Local Similarity 53.1%;
Matches 145; Conservative (
                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                             FILING DATE: 17
CLASSIFICATION:
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26 AGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCGT 85
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APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
AITLE OF INVENTION: DAS SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2.1
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53.1%; Pred. No. 1.7e-05;
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Search completed: March 16, 2004, 03:01:13
Job time : 82.7645 secs
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                               APPLICANT: Marc J. Rubenfield et al.
TITLE DE INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE DE INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR RELING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-7
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7571
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Patent No. 6476209
GENERAL INFORMATION:
APPLICANT: Glann, Matthew
APPLICANT: Lubbers, Mark W
APPLICANT: Dekker, James
TITLE OF INVENTION: Polymucleotides, materials incorporating
TITLE OF INVENTION: them, and methods for using them.
FILE REFERENCE: 104801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 107; Indels
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Pred. No. 2.9e-06;
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 124
SOFTWARE: FastERQ for Windows Version 4.0
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US-09-724-623-24
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Best Local Similarity 54.3%;
Matches 134; Conservative
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Patent No. 6551795
GENERAL INFORMATION:
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Best Local Si
Matches 176
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SEQ ID NO 24
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545 CGCGTTCCTGGGCGATGTCATTGAGCTTGCGGACCATATCAATATTGTTCACGTTCAACA 604
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                                                              934 GGTTATCCTGAAGGTGTTCAACTGAGGTCGTCCCAATGATCACACTTGTGACAA----- 881
                                                                                                                                                                                              712 Agcgarichganadadadcerichganaacgercestardeaarcegaceacear 656
                                                                                                                                                    485 CGCCGTACTCTCCTTGCTCGCGCACCCCATGCAAGCGCCCATCTGCGCAAGTGACTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            665 ATTIGICCGIGAGCAGGCCCIGCGCAAGIGGIGAGAAAGCAAIGACGCCAAGACCAI
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Sequence 1, Appli Sequence 19965, Ap Sequence 7020, Ap Sequence 33379, A Sequence 38764, A Sequence 1450, Ap Sequence 77, Appl Sequence 1109, Ap

Sequence 1, Appl.
Sequence 11, Appl.
Sequence 11, Appl.
Sequence 11, Appl.
Sequence 648, Appl.
Sequence 24, Appl.
Sequence 15, Appl.
Sequence 15, Appl.
Sequence 28453, A.
Sequence 31213, A.
Sequence 31213, A.
Sequence 21647, A.

31368, A 28610, A

ALIGNMENTS

39, Appl

Sequence Sequence Sequence Sequence Sequence Sequence

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15 US-10-369-493-37651

14 US-10-156-761-1151

US-10-282-122A-19965

12 US-10-282-122A-33379

12 US-10-282-122A-33379

12 US-10-282-122A-3379

12 US-10-282-122A-33764

15 US-10-282-122A-39389

16 US-10-282-122A-39764

17 US-10-282-122A-39764

18 US-10-156-761-1109

19 US-09-974-300-77

10 US-10-282-122A-21370

10 US-10-282-122A-21451

14 US-10-282-122A-41645

15 US-10-282-122A-41645

16 US-10-369-493-28453

15 US-10-369-493-28453

15 US-10-369-493-31213

16 US-10-369-493-31213

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19 US-10-369-493-31368

10 US-10-038-854-31

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                                                                                                                                 March 17, 2004, 00:51:03; Search time 312.967 Seconds (without alignments) 10269.549 Million cell updates/sec
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                                                                                                                                                                                                                                                 1 gtcgataagcagcgggtttg.......873
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1: \cgn2_6/ptodata/1/pubpna/USO7_pUBCOMB.seq:*

2: \cgn2_6/ptodata/1/pubpna/PCTTMW PUB.seq:*

3: \cgn2_6/ptodata/1/pubpna/USO6 NEW PUB.seq:*

4: \cgn2_6/ptodata/1/pubpna/USO6 NEW PUB.seq:*

5: \cgn2_6/ptodata/1/pubpna/USO7 NEW PUB.seq:*

6: \cgn2_6/ptodata/1/pubpna/USO7 NEW PUB.seq:*

7: \cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*

8: \cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*

9: \cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*

9: \cgn2_6/ptodata/1/pubpna/USO8_NEW Seq:*

10: \cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*

11: \cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*

11: \cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*

12: \cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*

13: \cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*

14: \cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*

15: \cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*

16: \cgn2_6/ptodata/1/pubpna/USIOB_NEW PUB.seq:*

17: \cgn2_6/ptodata/1/pubpna/USIO_NEW PUB.seq:*

18: \cgn2_6/ptodata/1/pubpna/USIO_NEW PUB.seq:*

18: \cgn2_6/ptodata/1/pubpna/USIO_NEW PUB.seq:*

18: \cgn2_6/ptodata/1/pubpna/USIO_NEW PUB.seq:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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9 US-09-738-626-3454
3 12 US-10-627-476-669
2 10 US-09-746-660A-51
1 14 US-10-166-142-9
1 4 US-10-166-142-9
8 9 US-09-738-626-3455
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Best Local Similarity 100.0%; Pred. No. 1.2e-272;
Matches 873; Conservative 0; Mismatches 0; Indel8 0;
TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                    ; LOCATION: (1025)..(1723)
; OTHER INFORMATION:
US-10-196-232-24
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Sequence 38826, A Sequence 38124, A Sequence 13437, A Sequence 14390, A Sequence 11887, A

US-10-282-122A-17521 US-10-369-493-35174 US-10-369-493-38124 US-10-369-493-38124 US-10-282-122A-14347 US-10-282-122A-14390 US-10-282-122A-11390

253.6 136.6 136.6 136.6 105.8 96.8

46.3 37.3 37.3 38.7 34.7 29.0 115.6 115.6 112.1 111.1

304.4

404.2 326 306

Sequence 3455, Ap Sequence 17521, A Sequence 35374, A 0

Gaps

180

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1328488 AACCCGAATGCGTATTTGGACGCGTTTGTGTTTATCGGCGCGCGTCGCCGCCCAATACGGC 1328429
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                                                                                                                                                                                                              100.0%; Score 873; DB 9; Length 3309400; 100.0%; Pred. No. 2.7e-271;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                            0; Mismatches
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 1
                                                                                                                                                      ; TYPE: DNA; OCKJNEBACTERIUM glutamicum
US-09-738-626-1
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Best Local Similarity 100.
Matches 873; Conservative
                                                                                                                                        LENGTH: 3309400
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APPLICANT: HAYASHI, MIKTRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: IKEDA, MASHIRO
APPLICANT: IKEDA, MASHIRO
APPLICANT: OZAKI, AKKO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: OTHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: IKEDA, MASATO
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Roopejus, Mark

APPLICANT: Roopejus, Mark

APPLICANT: Schoder, Markhard

APPLICANT: Schoder, Markhard

APPLICANT: Schoder, Markhard

APPLICANT: Schoder, Markhard

APPLICANT: Schoder, Markhard

APPLICANT: Schoder, Markhard

APPLICANT: Haberhauer, Gregor

TITLE OF INVENTION: TRANSPORT

FILE OF INVENTION: TRANSPORT

FILE OF INVENTION: TRANSPORT

FILE OF INVENTION: TRANSPORT

FILE OF INVENTION NUMBER: US/10/627,476

CURRENT FILING DATE: 1999-07-08

PRIOR PRICATION NUMBER: US 09/602,787

PRIOR PELICATION NUMBER: US 1999-07-08

PRIOR PELICATION NUMBER: DE 19931454.3

PRIOR PELICATION NUMBER: DE 19931454.3

PRIOR PELICATION NUMBER: DE 1993-07-08

PRIOR APPLICATION NUMBER: DE 1993-122.1

PRIOR APPLICATION NUMBER: DE 1993122.1

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PRIOR PELING DATE: 1999-07-09

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 AGCACCAATCAATGCACTGGTCACGGTA--TCCGCGCCGTACTCTCCTTGCTCGCGCAGC 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         511 ACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGCGTTCCTGGGCGATGTCATTGAGC 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                933 ACCCAIGCAAGCGCCAICTGCGCAAAGTGACTGCCCGCGTTCCTGGGCGATGTCATTGAGC 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 571 TIGGGGGCCATATCAATATIGTICACGTICAACATGCCCTCAGACAGGGACTTACCCTGG 630
207 GGCAGCTGACTGCAACATGTCTCACCGTCATCGCCCGGTTCCTCCACCCAACGATTAAT 148
                                                                   786 GATGGAATAGCTTGGCTGATGAATCAGAAGCGGGCAGCCCTCCTCCGCCATGAACTCAGC 845
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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Pred. No. 1.7e-120;
0; Mismatches 3; Indels 2;
                                                                                                                                                                                                                 846 CGCCTCCGCTGTGAGCTCTGGACCGTAG 873
                                                                                                                                                                                                                                                              CGCCTCCGCTGTGAGCTCTGGACCGTAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 669, Application US/10627476; Publication No. US20040030116A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.8%;
Matches 418; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (101)..(970)
; OTHER INFORMATION: RXN03164
US-10-627-476-669
                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-627-476-669/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
                                                                                                                           g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   627 GITTICGCGGGTTTTGGAATCGGTGGTCTTCGCCCCAAATGTTGATGCCGGCGTCGTGGGA 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 AATCTCATCGATCGCCTCCAACTCGGCGTCAGAAACTCCAAGTTGTTGAGTGAATCAAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 GCCGTACTCTCCTTGCTCGCGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCC 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447 GCCGTACTCCCTTGCTCGCCCAGCACCCATGCAAGCGCCCATCTGCCGCAAGTGCAAGTGCCC 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         546 GCGTTCCTGGGCGATGTCATTGAGCTTGCGGACCATATCAATATTGTTCACGTTCAACAT 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 GCGTTCCTGGGCGATGTCATTGAGCTTGCGGACCATATCAATATTGTTCACGTTCAACAT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   606 GCCCTCAGACAGGGACTTACCCTGGCTGGCGGGGAACCCTCTGGAATTCCATCGAGATA 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 GCCCTCAGACAGGGACTTACCCTGGCTGGCGGGAACCCTCTGGAATTCCATCGAGATA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITIGICCGIGAGCAGGCCCIGCGCAAGTGGIGAGAAAGCAAIGACGCCAAGACCATIGIT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 TITIGICCGTGAGGCCCTGCGCAAGTGAGAAAGCAATGAGGCAATGACGATTGTT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  567 AATCTCATCGATCGCCTCCAACTCGGCGTCAGAAACTCCAAGTTGTTGAGTGAATCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 GITTICGCGGGTTTIGGAAICGGTGGCCTICGCCCAAATGITGAIGCCGGCGICGIGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                              1327708 TCAGCCGCCTCCGCTGTGAGCTCTGGACCGTAG 1327676
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MACGUCHI, HINOSHI
APPLICANT: MACGUCHI, HINOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: AKOO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TITLE OF INVENTION NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: J9 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SOFTWARE: PATENTIN NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
SOFTWARE: PATENTIN NUMBER: JP 00/280989
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 3454
LENGTH: 627
                                         841 TCAGCCGCCTCCGCTGTGAGCTCTGGACCGTAG
                                                                                                                                                                                                                                                                                 Sequence 3454, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum
                                                                                                                                                                                                                                                           US-09-738-626-3454/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-738-626-3454
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Sequence 7, Application US/10166142

| Publication No. US2003124687A1
| Publication No. US2003124687A1
| GENERAL INFORMATION:
| APPLICANT: YASUEDA, HISASHI
| TITLE OF INVENTION: ASSIMILATING BACTERIUM
| FILE REPRENCE: 223789US
| CURRENT FILING DATE: 2002-06-11
| FRICK REPRENCE: 223789US
| CURRENT FILING DATE: 2002-06-12
| FRICK REPRENCE: 2002-06-12
| FRICK FILING DATE: 2001-06-12
| FRICK FILING DATE: 2001-06-12
| SEQ ID NO: 106-12
| SEQ ID NO 7
| LENGTH: 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406 GICGAIAAGCAGCAGGITITGGGTAAAGCCCAIGITGATGGCAATCGIGCTGACCIGGTIG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 CTGGTGGGTTTCGGCGCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCCAAGGTGTGGCGC 240
                                                                                                                                                                                                                                                                                                                                              61 AACCCGAATGCGTATTTGGACGCGTTTGTGTTTTATCGGCGGCGTCGGCGCGCAATACGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AACCCGAATGCGTATTTGGACGCGTTTGTGTGTTTATCGGCGGCGTCGGCGCGCAATACGGC 120
                                                                                                                                                                                                                                   617 GACACCGGACGGTGGATTTTCGCCGCTGGCGCTTCGCGGCAGGCTGATCTGGTTCCCG 676
                                                                                                                                                                                                                                                                                                                                                                                                                            241 TGGATCAACGTCGTCGTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATG 300
497 GTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTG 556
                                                                                       121 GACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGCCAAGCCTGATCTGGTTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CTGGTGGGTTTTCGGCGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 GGTTAGTTTTCGCGGGTTTTGGAATC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        797 GGTTAGTTTTCGCGGGTTTTTGGAATC 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Brevibacterium lactofermentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(711)

CTHER INFORMATION:

US-10-166-142-7
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NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-10-166-142-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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                                                                                                                                                                                  691 AGTGGTGAGAAAGCAATGACGCCAAGACCATTGTTGGCAGCTGACTGCAACAAGTTCTCA 750
                                                                                                                                                                                                                                CCGTCATCGCCCGGTTCCTCCACCCAACGATTAATGATGGAATAGCTTGGCTGATGAATC 810
                                                                                                                                                                                                                                                                                                                                              693 CCGTCATCGCCCGGTTCCTCCACCAACGATTAATGATGGAATAGCTTGGCTGATGATGATC 634
                                                                                                                                                                                                                                                                                                                                                                                                                               811 AGAAGCGGGCAGCCCTCCTCCGCCATGAACTCAGCCGCCTCCGCTGTGAGCTCTGGACCG 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         633 AGAAGCGGGCAGCCCTCCTCCGCCATGAACTCAGCCCTCCGCCTGTGAGCTCTGGACCTCTGGACCT
                                                          631 CTGGCGCGGGAACCCTCTGGAATTCCATCGAGATATTTGTCCGTGAGCAGGCCCTGCGCA 690
   873 TIGCGGACCATATCAATATTGTTCACGTTCAACATGCCCTCAGACAGGACTTACCCTGG 814
                                                                                                       1 GTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTG
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APPLICANT: Rooper', Burkhard
APPLICANT: Schroder', Hartwig
APPLICANT: Schroder', Hartwig
APPLICANT: Schroder', Hartwig
APPLICANT: Schroder', Hartwig
APPLICANT: Schroder', Hartwig
APPLICANT: Haberhauer', Gregor
APPLICANT: Haberhauer', Gregor
APPLICANT: Hamang, Bung-Joon
ITITLE OF INVENTION: CORNUBBACTERIUM GLUTAMICUM GENES ENCODING
ITITLE OF INVENTION: WATABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CP2
CURRENT APPLICATION NUMBER: US/09/746,660A
CURRENT APPLICATION NUMBER: 09/603124
PRIOR APPLICATION NUMBER: 09/14031
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-25
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PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-35
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-03
PRIOR PILING DATE: 1999-07-08
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37.3%; Score 326; DB 10; Length 822;
Best Local Similarity 100.0%; Pred. No. 3.9e-95;
Matches 326; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: RXA01394
US-09-746-660A-51
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US-09-746-660A-51
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Best Local Similarity 100.0%; Pred. No. 1.1e-87;
Matches 303; Conservative 0; Mismatches 0;
      APPLICANT: OZAKI, AKKO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERRACE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
FRIOR APPLICATION NUMBER: UP 99/377484
FRIOR APPLICATION NUMBER: UP 00/159162
FRIOR PLICATION NUMBER: JP 99/377484
FRIOR PLICATION NUMBER: JP 00/159162
FRIOR PLICATION NUMBER: JP 00/280989
FRIOR FILING DATE: 2000-08-03
FRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 3455
LENGTH: 708
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17521, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Corynebacterium glutamicum
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Zyskind, Judith
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APPLICANT: GUNJI, YOSHIYA
APPLICANT: GUNJI, YOSHIYA
APPLICANT: YASUEDA, HISASHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL
TITLE OF INVENTION: ASSIMILATING BACTERIUM
FILE REFERENCE: 223789US
CURRENT APPLICATION NUMBER: US/10/166,142
CURRENT PELLING DATE: 2002-06-11
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 10
SOFWARE: PATENTIN VERSION 3.1
SEQ ID NO 9
LENGTH: 712
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Pred. No. 3.8e-88;
0; Mismatches 1
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Sequence 3455, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: ANTOGONIH, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIA!, KEIKO
APPLICANT: YOKO!, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
                                                                                                                                       ; Sequence 9, Application US/10166142; Publication No. US20030124687A1
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99.7%;
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Best Local Similarity 99.7
Matches 305; Conservative
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301 GGTTAG 306
                                 706 GGTTAG 711
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OTHER INFORMATION:
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LOCATION: (1)
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/203-02-28
PRIOR APPLICATION NUMBER: US/203-02-28
PRIOR APPLICATION NUMBER: US/203-02-28
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RIOR APPLICATION NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-369-493-38826/c
; Sequence 38826, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
Sequence 35374, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Agrobacterium tumefaciens US-10-369-493-35374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.6
Best Local Similarity 56.8
Matches 312; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         865 GGACCGTAG 873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGACTGCAACAAGTTCTCACCGTCATCGCCCGGTTCCTCCACCCAACGATTAATGATG 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATAGCTTGGCTGATGAATCAGAAGCGGGCAGCCCTCCTCCGCCATGAACTCAGCCGCC 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 614 GAATAGCTCGGTTGATGAATCAGCAGCGGGGGGCCTCACCAGCTAGAATTTCCGAGATC 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 TCGCGGGTTTTGGAATCGGTGGCCTTCGCCCAAATGTTGATGCCGGCGTCGTGGGAAATC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 TCAGACAGGGACTTACCCTGGCTGGCGCGGAACCCTCTGGAATTCCATCGAGATATTG 669
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   PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
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PRIOR PLING DATE: 2000-12-22
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PRIOR PLING DATE: 2001-02-09
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PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/250,308
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PRIOR APPLICATION NUMBER: 60/250,308
PRIOR APPLICATION NUMBER: 60/250,308
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-03-16
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Pred. No. 1.5e-71;
0; Mismatches 194; Indels
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Best Local Similarity 65.67
Matches 370; Conservative
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384

Gaps

963 444 903 504 861 564 801 624

684

RESULT 10 US-10-369-493-35374/c

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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE REPREBENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-022-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PRIOR DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NOS: 47374
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15.6%; Score 136.6; DB 15; Length 1028;
Best Local Similarity 56.8%; Pred. No. 1.5e-33;
Matches 312; Conservative 0; Mismatches 204; Indels 33;
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; Sequence 13437, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Maxlone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGACCGIAG 873
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                      APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION UNMERR: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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Matches 312; Conservative
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LENGTH: 1026
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11.1%; Score 96.8; DB 12;
Best Local Similarity 56.9%; Pred. No. 1.3e-20;
Matches 232; Conservative 0; Mismatches 152;
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-12
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,335
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
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Publication No. US20040029129A1
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Sequence 1%...

Bublication No. Us...

GENERAL INFORMATION:

APPLICANT: Wang, Liangeu

APPLICANT: Anno, Carlos

APPLICANT: Haselbeck, Robert

APPLICANT: Malone, Cheryl

APPLICANT: Ollsen, Kari

"NT: Zyskind, Judith
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SOFTWARE: PatentIn version 3.1
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Carr, Grant
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                                                                                                                                                  TITLE OF INTENTION: H. H. TITLE OF INTENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
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                                         Yamamoto, Robert
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                                     567 GAGCITGCGGACCATATCAATATTGTTCACGTTCAACATGCCCTCAGAGCAGGGACTTACC 626
                                                                                 -----CIGGCIGGCGCGCGGAACCCICGGAATICCAICGAGAIAITIGICCGIGAGCAG 680
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PRIOR APPLICATION UNDERS: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-10-29

PRIOR PILING DATE: 2000-10-29

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-27

PRIOR FILING DATE: 2000-12-27

PRIOR FILING DATE: 2000-12-27

PRIOR FILING DATE: 2001-20-29

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

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PRIOR FILING DATE: 2001-02-16
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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Best Local Similarity 55.7%; Pred. No. 1.9e-20;
Matches 241; Conservative 0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11887, Application US/10282122A Publication No. US20040029129A1
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Zyskind, Judith
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US-10-282-122A-11887/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
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AF075981 AP075981 Salmonella typhimurium LT2, Lambda DASH II Salmonella typhimurium genomic clone 390-T3, genomic survey sequence.
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AA55288 zx41c05.8
W1050 mE83h05.r1
AA46580 zx02h03.s
A1159901 qb55h08.x
CG694695 zwBBbb029
A1401605 tf60b01.x
A18280014 wj60401.x
A1828014 wj60401.x
A1828014 UI-W-FY0-BZ89455 Hg1_0107
AX011268 Mws mwscu
AX011268 Mws mwscu
AX405421 Pan trogl
AX405421 Pan trogl
AX05420 Homo sapi
AX07777 B Drosophil
AL07773 Drosophil
AL073319 Drosophil
AX51080 BX361080
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         AL247708 Tetraodon
BH770958 LLMGtag68
BE574094 msh2 3508
BX424825 BX424625
BY246241 BY246241
CD861975 AZO1.101N
BM712036 UI-E-DW1-
BUZ20119 603743368
BM729055 UI-E-DO1-
BE898495 601681396
BE740880 601593311
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1 (bases 1 to 860, Wong, K.K., Benson, N.R. and McClelland, M. Sample sequencing of a Salmonella typhimurium LT2 lambda library: comparison to the Escherichia coli K12 genome FEMS Microbiol. Lett. 173 (2), 411-423 (1999)
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Sidney Kimmel Cancer Center
3099 Science Park Road, San Diego,
Email: mcclelland@lifeci.edsu.edu
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                                                       BX424825
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Location/Qualifiers
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Salmonella typhimurium
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AUTHORS
TITLE
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PUBMED
COMMENT
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KEYWORDS
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BZ568946 pacs2-164
AL108460 Drosophil
                                                                                                   March 15, 2004, 13:43:00 ; Search time 2400.75 Seconds (without alignments) 10858.975 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                        27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                 US-09-105-117K-1_COPY_1421_2293
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Maximum Match 100%
Listing first 45 summaries
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BZ560550
BZ568946
CNS017SY
                                                                       - nucleic search, using sw model
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Gaps

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BZ568946 11-DEC-2002 pacs2-164_8165.y2 pacs2-164_8165 acroginosa genomic clone pacs2-164_8165, genomic survey sequence.
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/strain="2-164"
/db_xref="taxon:287"
/clone="pacs2-164 2569"
/clone=lb="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun library."
                                                                                                                                                                                                                                                                                                                                                       Query Match 6.2%; Score 54.2; DB 28; Best Local Similarity 52.8%; Pred. No. 0.035; Matches 143; Conservative 0; Mismatches 120;
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                                                                                                                                                                                  /clone="399-T3"
/clone lib="Salmonella typhimurium LT2, Lambda DASH II"
/note="Vector: Lambda DASH II; sequenced using Li-Cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Burns, J. L., Kaul, R. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56.4; DB 28; Length Pred. No. 0.01; 0; Mismatches 151; Indels
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/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
                          /organism="Salmonella typhimurium"
/mol_type="genomic DNA"
/strain="ITZ"
/db_xref="taxon:602"
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University of Washington
Box 351145, Seattle, WA 98105-2145, USA
Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 2066857244
Email: craymond@u.washington.edu
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Contact: Chris K. Raymond
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Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.B., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:287"
/clone="pacs2-164 8165"
/clone lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
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                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                       Genome Center
Inversity of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                 Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="2-164"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pseudomonas
                             Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1620)
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CD881613 720 bp mRNA linear EST 14-JUL-2003 F1.103L23F010329 F1 Triticum aestivum cDNA clone F1103L23, mRNA
                                               899 BTKSTSSTSSSSTBETTTSBESSSSSSSSSTTTTSBSSTBSSYGSSSBTCTSKCSTB 840
                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Triticum.
1 (bases 1 to 720)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CTGGTGGGTTTCGGCGCAGCAGTTGTCACGCCCGCTGTCCAGCCCCCAAGGTGTGGCGC 240
                  252 CGTCGTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATGGGTTAGTTTTC 311
                                                                                                        312 GCGGGTTTTGGAATCGGTGGCCTTCGCCCAAATGTTGATGCCGGCGTCGTGGGAAATCTC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 GTGGAGGAGAAGCTGGTGGCGCTCAAGCCCAAGAGCATCGACTTCGCGCAGGCCGCCGCT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 creccecroeccarceadacceccareaesecriceaeaeseseseseserrerececcese 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 AAGTCCATCCTCGTCCTCGGCGGCGCGGCGGAGTCGGGACCCTCGTCATCCAGCTGGCG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               432 AAGCAAGTTTACGGCGCGCGTCGACGGTGGCGGCCACCAGCACCCCGGAAGCTGGAGCTC 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATGGTGGTGACCTGGTTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 I 69 47 54 00
Fax: 33 I 69 47 54 10
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/mol_type="mRNA"
/cultivar="recital"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:4565"
/clone="F1103L23"
/tissue_type="leaf one"
/clone_lib="F1"
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Pred. No.
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                                                                                                                                                                                                                          372 ATCGATCGCCTCCAACTCGGCGTC 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum
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CD881613
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDCP) - thtp://www.edpp.ebi.ac.uk - This Drosophila melannogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 GTATTTGGACGCGTTTGTGTTTATCGGCGCGTCGGCGCGCAATACGGCGACACCGGACG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 GIGGATITICGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGGTTT 191
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                                          122 ACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGC 181
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Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37L08 of DrosbAC library from Drosophila melanogaster (fruit
                                                                                     618 AGNCCGCGCCCGCGCGCATATGCCCTCGGCGCCGCCCACGCCTCGATGATGTGGTTCTTCG
                                                                                                                                  182 TGGTGGGTTTTCGGCGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCT
                                                                                                                                                                                                                       242 GGATCAACGTCGTCGTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATGG
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0; Gaps
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea; Drosophilidae, Drosophila.
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84; Indels
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0; Mismatches
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/db xref="taxon:7227"
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/clone lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fly), genomic survey sequence.
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Matches 100; Conservative
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                                                                                                                                                                                                                                                                                     GSS 01-MAY-2002
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458 GAGGCTCCCCCACGGTGGARCCTCCCCGGCCGTGGAGGCTCCCCCCCGTGGTGGGGTCTT 517
                                                                                                                                                                                                                                                                                                             LIMGtag686 MG1363 Random Sequence Tag Library Lactococcus lactis
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Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments (2002) In press
Contact: Sorokin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.0%; Score 43.8; DB 28; Length 3237; Best Local Similarity 49.9%; Pred. No. 22; Matches 170; Conservative 0; Mismatches 162; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Lactococcus lactis subsp. cremoris"
                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                     subsp. cremoris genomic, genomic survey sequence.
BH770958
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Fax: 33 i 34 65 25 21
Email: sorokine@jouy inra.fr
best homologue in strain II1403 is 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis subsp. cremoris
Lactococcus lactis subsp. cremoris
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/strain="MG1363"
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                                                                                                                           Terración nigroviridis genome survey sequence T7 end of clone 032806 of library G from Tetracdon nigroviridis, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                          GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Talsostei; Buteleostei; Neoteleostei;
Actinoptay; Accenthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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/note="Genoscope sequence ID : COBG032DA03LP1~end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence NAT. Genet. 25 (2), 235-238 (2000)
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="03286"
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 TCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGTTCCGCCGCAGCAGCATTGTCACGCC
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                    Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Bmail: Sequescope.cns.fr,
Bmail: sequescope.cns.fr,
Library was constructed by Life Technologies, a division of
Intitrogen. Contact. Feng Liang Email : filiangelifetech.com U
http://fulllength.invitrogen.com/ Invitrogen.com/ Invitrogen.com/ Secuence ID : XCLOBA001ZE02FPI.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                     'organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
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Unpublished (2001)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    527 cercercescerrereacesacacescesces de actives de concerce de concese de concerce de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de concese de co
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                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas acruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadacea;
I (base 1 to 1955)
Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, E. E., Hastings, M., Burns, J. L., Kaul, R. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
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XCLOBA001ZE02 3-PRIME, mRNA sequence.
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Pred. No. 20;
0; Mismatches 68; Indels 0;
   2253 AGTCCTTGATACAAAGGCTTAAAGGCAATTGTTCCTATCCC 2293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Box 352145, Seattle, WA 98105-2145, USA
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/clone="msh2_3508"
/clone_lib="msh"
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Homo sapiens
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Best Local Similarity 55.39
Matches 84; Conservative
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BX424825/c
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BZ574094/c
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CD861975 538 bp mRNA linear EST 11-JUL-2003 AZO1.101N14F010125 AZO1 Triticum aestivum CDNA clone AZO1101N14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (bases I to 538)
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200 CCTGTGCCTCCGCCACAGAAAGCTCAGTGCTGGAAGACAGGTGGCTGGTATTCGGAC 141
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
Finis sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Contact: Genoplante
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                                                                                                                                      440 GCTCAACTGACGAAGCACCAATCAATGCACTGGTCACGGTATCCGCGCCGTACTCCCTT
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0; Mismatches 142; Indels
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/clone_lib="AZ01"
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                                              Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Percole,G., Ramachandran,S., Ravasi,T., Reid,J., Rang, Pesole,G., Ramachandran,S., Ravasi,T., Redd,J.C., Reid,J.C., Ramachandran,S., Ravasi,T., Reed,D.J., Reid,J. Ring,B.Z., Ringwald,M., Sultana,R., Takengier,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenara,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wallenger,L., Wahlbertedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw,Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yang,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Arawasi,J., Aizawa,T., Arakawa,T., Pukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,A., Yasuishi,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasuishi,A., Yoshino,M., Waterston,R., Lander,B.S., Rogers,J., Birney,E. and Hayashizaki,Y. Rasaki,C., Lander,B.S., Narayasis of the mouse transcriptome based on functional annotation of 60,707 (2011-1904)
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URL:http://genome.gec.riken.go.jp,
URL:http://genome.gec.riken.go.jp,
Aizawa.K., Akimura.T., Arakawa.T., Itoh,M., Kawai.J., Konno,H.,
Hirozane,T., Imorani,K., Ishii,Y., Itoh,M., Kawai.J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakarume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected CDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
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Tissues were provided by Michela Fagiolini and Takao K. Hensch (
Tissues were provided by Michela Fagiolini and Takao K. Hensch (
Laboratory for Neuronal Circuit Development Brain Science Institute
RIKEN 2-1 Hirosawa, Wako-shi, Saitama 351-0198 Japan ) whose
assistance we gratefully acknowledge. Please visit our web site
(http://genome.gsc.riken.go.jp) for further details.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchitro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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                           Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
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51.6%; Pred. No. 22;
tive 0; Mismatches 90; Indels
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289 AAGCAAGTTTACGGCGCATCGAAAGTGGCGGCCCACAGCCCAGCACCCCAAAGCTGGAGCTC 348

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Gaps

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380 CCTCCAACTCGGCGTCAGAAACTCCAAGTTGTTGAGTGAATCAAGGCTGTTGTCCAGCT 439

96; Conservative

Matches

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Query Match Best Local Similarity

241 TGGATCAACGTCGTCGTGGCAGTTGTGAT 269

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/note="Organ: whole embryo; Vector: pBluescript II KS(+);
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
/note="Constructed from I million independent clones. cDNA
/notehylated C in the first strand synthesis reaction.
/notehylated C in the first strand reaction, double-stranded cDNA
/notehylated Lists strand reaction, double-stranded cDNA
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/note I is a custom modified MCS of the
/note pBluescript (KS+) vector. The library was normalized in 2
/note in your conditions adapted from Soares et al., PNAS
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi,
Archosauria, Aves.
Archosauria, Aves.
In (Bases 1 to 588)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                            158 CGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGCGCCAGCAGCATTGTCACGCCCGC 217
                                                                                                                                                       472 ccaccorgoridaacridaaacacacarcacorraaridaacacrrrrcaacaccorradagaccec 413
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University of Manchester Institute of Science and Technology
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/organism="Gallus gallus"
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
Coordinated Laboratory for Computational Genomics
University of Lowa
375 Newton Road (4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9626
Fax: 319 335 9626
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com)
The following respectitive elements were found in this CDNA
sequence: 143-166, >9C. Tich#Low_complexity
                                                                                                                                                                                                                                                                                               BM712036 558 bp mRNA linear EST 28-FEB-2002 UI-E-DW1-ahc-g-16-0-UI.rl UI-E-DW1 Homo sapiens cDNA clone UI-E-DW1-ahc-g-16-0-UI 5', mRNA sequence.
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-DW1"
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/db_xref="taxon:9606"
/clone="Ul-E-DW1-ahc-g-16-0-Ul"
/tissue_type="lens"
349 CTGAAAAGCCTGGGAGCCGACGTCGCCAT 377
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BM712036.1 GI:19025294
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/tissue_type="fetal eye"
/dev stage="fetal"
/lab_host="HH108 (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-E01"
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The following repetitive elements were found in this cDNA sequence: 148-171, SC richHow.complexity
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                                                                                                                                              517 CCACGCCGGACATTCACAGCTGGCCCCGGGCGCACGCACTGTCACCGTCACCGCGTCACT 458
                                                                                                                                                                                            542 GCCCGCGTTCCTGGGCGATGTCATTGAGCTTGCGGACCATATCAATATTGTTCACGTTCA 601
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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University of lowa
The Newton Road , 4156 MEBRF, lowa City, IA 52242, USA
Tel: 319 335 9565
Fax: 319 335 9565
Score 41.6; DB 13; Length 588;
                                                 74; Indels
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                                                                                                                                                                                                                                                                                              602 ACATGCCCTCAGACAGGGACTTACCCTGGCTGGCGCGGGA
Query Match 4.8%; Score 41.6; UB Best Local Similarity 53.8%; Pred. No. 31; Matches 86; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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BM729055.1 GI:19050388
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Homo sapiens
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BEB98495 1710 bp mRNA linear EST 29-SEP-2000 601681396F1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3951622 5',
sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 770)
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov
Flaute: LLCM819 row: p column: 23
High quality sequence stop: 765.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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46.9%; Pred. No. 45;
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/lab_host="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
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Homo sapiens
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Best Local Similarity 46.99
Matches 128; Conservative
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California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

98 ececcorcececannacececanacecenteres 157 385 GCAGGCCCAGCGCCGAACTGCATCTCCACGTCCGCGAACCTGCGCGTCCTGCCGTTCA 326 158 CGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGCGCCAGCATTGTCACGCCCGC 217 325 CCACCGTGGTGGACTGCGACACGTCACGTTGATGCCGTTCTCCAGCGCCTTGCGGCCGC 266 218 TGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTGGCAGTTGTGATGACCGCAT 277 265 TGCTCAACCGCAGCGTGCCCAGGTCGCTCTCGGGCGTGGTCTTGATGAAGTAGTGCG 206 278 TGGCCATCAAACTGATGTTGATGGTTAGTTTTCGCGGGTTTTTGGAATCGGTGGCCTTCG 337 205 TGTCCTTGCCCTCGATGGTGAAGTGCAGGTTCTCCCAGGTAGAAGGCGTTGTTGAGCACGG 146 0; Gaps Query Match
Best Local Similarity 46.9%; Pred. No. 50;
Matches 128; Conservative 0; Mismatches 145; Indels 145 CCGCCACCTTGATGCAGTCCTCGTTGGCGATGT 113 338 CCCAAATGTTGATGCCGGCGTCGTGGGAAATCT 370 q ö δ qq ð g qq δ Š

Search completed: March 16, 2004, 02:52:18 Job time : 2403.75 secs

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March 12, 2004, 18:03:00 ; Search time 60 Seconds (without alignments) 1111.354 Million cell updates/sec
                                                                                                                                                                                                                                         1 MVIMEIFITGLLIGASLLLS.....INVVVAVVMTALAIXUMLMG 236
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		**			SUMMARIES	
Result	0	Query	Query	ĝ	Ę	المنتمون
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П	1191	100.0		~	AAW37715	O
7	1191	100.0		4	AAG93201	ບ
е	1191	100.0	236	9	ABR58213	Н
4	1178	98.9		4	AAB79660	Aab79660 Corynebac
S	1178	98.9		4	AAU71888	Aau71888 C. glutam
9	1178	98.9		7	ADB66197	Adb66197 Protein e
7	864.5	72.6		4	AAG64047	Aag64047 Corynebac
8	584	49.0		9	ABR58214	
6	350	29.4		٣	AAB01789	Aab01789 Escherich
10	298	25.0	208	9	ABM68839	
11	298	25.0		9	ADA34450	Ada34450 Acinetoba
12	170.5	14.3	210	~	AAW20426	
13	170.5	14.3	215	~	AAW20968	Ë
14	164	13.8	205	9	ABM72206	
15	132.5	11.1	205	9	ABM67507	
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17	121.5			9	ADA36962	
18	119.5	_	173	'n	ABP39181	Abp39181 Staphyloc
19	119.5	10.0		9	ADA35184	
20	119	٦	620	9	ABU49694	Abu49694 Protein e
21	114.5			m	AAB11637	
22	112	9.4		9	ABM70439	Abm70439 Photorhab
23	108.5			9	ABM68944	Abm68944 Photorhab
24	108.5	9.1	238	9	ADA35835	Ada35835 Acinetoba
25	105	8.8	206	m	AAY99598	Aay99598 E. coli L

Protein e Protein e C glutam E glutami Escherich Herbicida Corynebac C glutami	Abb28648 Abu19902 Abu79903 Abp93244 Abb93711 Abb93711 Abb9776722 Aag92602	ABU28648 ABU19902 AABT9897 AAB01786 ABB01786 AAB93711 AAB76702 AAG92602	ሱሱ 4 4 6 10 4 4 10	4444 6022444 60224444 60224444 60224444	C C C C C C C C C C C C C C C C C C C	93.5 92.1.9 92.1.5 91.5	C
E. coli c Protein e	Aau34590 Abu28648	AAU34590 ABU28648	4.0	452	9.7	93.5	36
Propionib Acinetoba	Abm54748 Ada36250	ABM54748 ADA36250	99	390	9.0	95 9 4 .5	34 35
Protein e Propionib	Abu49858 Aau58229	ABU49858 AAU58229	9 4	390	0 0 0 0	95 95	33
Acinetoba Photorhab	Ada33824 Abm67782	ADA33824 ABM67782	99	208 213	8 8 . 4	66 66 66	30 31
Photorhab Escherich	Abm68999 Aab01787	ABM68999 AAB01787	9 6	201	ອອ ຕິດ	101	28 29
Protein e Acinetoba	Abu16949 Ada33616	ABU16949 ADA33616	99	181	8.5	103.5	26 27

ALIGNMENTS

Sequence 236 AA;

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                                                                                                                                                                                                               AVAIDIRNRVRVEVSVDKQRVWVKPMLMAIVLIWLNPNAYLDAFVFIGGVGAQYGDIGRW 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                               DLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGS
                                                                      1 MVIMBIFITGLILGASLLLSIGPONVLVIKOGIKREGLIAVLLVCLISDVFLFIAGTLGV
                                                                                            61 DLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGS
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                                     Gaps
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Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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 Length 236;
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                                   Indels
100.0%; Score 1191; DB 2; 100.0%; Pred. No. 4.6e-128;
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                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C glutamicum protein fragment
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2000JP-00159162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                Best Local Similarity 100. Matches 236; Conservative
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Tateishi N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel DNA encoding variant of LysE protein from a coryneform bacterium,
                                                          1 MVIMBIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGV
                                                                           1 MVIMEIPITGLLIGASILLSIGPONVLVIKQGIKREGLIAVLVCLISDVELFIAGTLGV
                                                                                                                     61 DILISNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGS
                                                                                                                                      121 AVATDTRNRVRVEVSVDKQRVWVKPMLMAIVITWLNPNAYLDAFVFIGGVGAQYGDTGRW
                                                                                                                                                                                                                                                     181 IFAAGAFAASLIWPPLVGFGAAALSRPLSSPKVWRWINVVVAVWYALAIKLMLMG 236
                                                                                                                                                                                                                                      IFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVWTALAIKLMLMG 236
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        when introduced into methanol assimilating bacterium, facilitates excretion of L-lysine and/or L-arginine to outside of a cell.
                             0;
 Length 236;
                              Indels
100.0%; Score 1191; DB 4;
100.0%; Pred. No. 4.6e-128;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                           ABR58213 standard; protein; 236 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L-lysine; L-arginine; LsyE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum.
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                              Matches 236; Conservative
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                Local Similarity
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11-AUG-2003
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    Query Match
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184 AGAFAASLIMFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
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27-AUG-1999;
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                                                                                                                                                                                                                                                                             Corynebacterium glutamicum; metabolic pathway protein, MP protein, fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
                                              AVAIDIRNRVRVEVSVDKQRVWVKPMLMAIVLIWINPNAYLDAFVFIGGVGAQYGDTGRW
                                                                        DILISNAAPIVLDIMRMGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGS
                                     1 MVIMBIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGV
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                     Gaps
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   Length 236;
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                   Indels
  Score 1191; DB 6;
Pred. No. 4.6e-128;
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                   0; Mismatches
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 100.0%;
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                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum
                                                                                                                                                                                                                                             (first entry)
                 Matches 236; Conservative
Query Match
Best Local Similarity
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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleosides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids from Corynebacterium glutamicum encoding metabolic pathw
proteins, useful for producing fine chemicals in microorganisms,
including organic acids, nonproteinogenic amino acids, and purine and
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                                                                                                                            990S-0148613P.
990E-01040764.
990E-01040765.
990E-01040766.
990E-01040832.
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99DE-01042076.
99DE-01042077.
99DE-01032926.
                                                       99DE-01033004.
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99DE-01(
99DE-01(
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63 9 120 183 180 181 AGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVWTALAIKLMLMG 233

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The present invention relates to the isolation of novel Corynebacterium glutamicum genes (AAS96073-AAS96132) encoding metabolic pathway (MP) proteins. The metabolic pathway proteins of the invention include enzymes involved in the lysine and methionine biosynthetic pathways. The polymucleotide sequences of the invention can be used for the large-scale production and/or modulation of expression of fine chemicals such as lysine and methionine. The sequences of the invention may be used to identify C. glutamicum and related organisms e.g. C. diphtheriae in a subject to detect diphtheria. AAU71863-AAU71922 represent the novel C. glutamicum metabolic pathway proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVA 123
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                                                                                                                                                                                                                                    Metabolic pathway protein; MP; lysine biosynthesis pathway;
methionine biosynthesis pathway; large-scale production of fine chemical;
Corynebacterium diphtheriae; diphtheria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEIFITGLILGASLILSIGPQNVIVIKQGIKREGLIAVLIVCLISDVELFIAGTLGVDLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding metabolic pathway proteins from Corynebacterium
glutamicum, useful for producing methionine and lysine in Corynebacterim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 MEIFITGLLIGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL
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181 AGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 233
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                                                                                                                                                                                                    glutamicum metabolic pathway protein encoded by gene #23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                          Ā
                                                                                          AAU71888 standard; protein; 233
                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-2000; 2000WO-IB002035.
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23-JUN-2000; 2000US-00606740.
                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum.
                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee H, Hwang
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                                                                                                                                                                   26-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2001
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                                                                                                                              AAU71888;
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The present invention relates to a method for producing L-arginine in a microorganism (e.g. coryneform bacteria) that has L-arginine producing ability and has been modified for enhanced expression of the lyeB gene. The microorganism is also modified so that an arginine repressor (argR) does not function normally. The method of the invention is useful for the enhanced production of L-arginine which is useful in liver function promoting agents, amino acid infusion and comprehensive amino acid pharmaceuticals. The present sequence represents a protein encoded by the Corynebacterium glutamicum LyAB gene. Note: The present sequence is given as SEQ ID Note: In the Sequence Listing but is referred to as SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A microorganism comprising enhanced expression of the lysE gene is useful for enhanced production of L-arginine.
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                                                                                                                                                 L-arginine production; coryneform bacteria; lysE; arginine repressor; argk; liver function promoting agent; amino acid infusion; amino acid pharmaceutical.
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tive 0; Mismatches
                                                                                                                          Protein encoded by C. glutamicum LysE gene
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                               Ā
                               ADB66197 standard; protein; 233
                                                                                                                                                                                                                                                                                                                                                                                                             Gunji Y,
                                                                                                                                                                                                                                                                                                                   17-JUL-2002; 2002US-00196232
                                                                                                                                                                                                                                                                                                                                                25-JUL-2001; 2001JP-00224586
                                                                                                                                                                                                                     Corynebacterium glutamicum.
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Best Local Similarity 100.1
Matches 233; Conservative
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                              (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                                                                                                                                                                                                                             Yamaguchi M, Ito H,
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-708853/67.
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                                                                                            04-DEC-2003
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                                                             ADB66197;
RESULT 6
ADB66197
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RESULT 7 AAG64047

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The present invention relates to DNA encoding variants of protein with loop region and six hydrophobic helixes which facilitates excretion of L-lysine and/or L-arginine to outside of cell of a methanol assimilating bacterium when introduced into the bacterium. The methanol is used for both of these L-amino acids to outside of a cell of a methanol assimilating bacterium when DNA of the methanol is introduced into the bacterium. The present sequence represents a lysE24 protein from Erevbacterium lactofermentum. (Updated on 23-0CT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DILSNAAPIVLDIMRWGGIAYILWFAVWAAKDAMTNKVEAPQIIEETEPTVPDDTFLG 118
                                                                                                                                                                                                                                                                                                                                                                                                    Novel DNA encoding variant of LysE protein from a coryneform bacterium, when introduced into methanol assimilating bacterium, facilitates excretion of L-lysine and/or L-arginine to outside of a cell.
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amino acid excretion protein.
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                L-lysine; L-arginine; LysE24.
                                                                                                                                                                                                                    12-JUN-2001; 2001JP-00177075.
                                                                                                                                                                              05-JUN-2002; 2002EP-00012539.
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                                                         Corynebacterium glutamicum.
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                                                                                                                                                                                                                                                            (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                Gunji Y, Yasueda H;
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                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ACC80942
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                                                                                               EP1266966-A2
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                                                                                                                                       18-DEC-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a gene from a high temperature-resistant coryneform microbe that encodes a heat-resistant lyain biosynthetic enzyme. The enzyme has aspartate-semialdehyde dehydrogenase activity and can be used for growing anino acid-producing microbes. The present amino acid sequence corresponds to an enzyme of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 SNAAPIVLDIMRWGGIAYLLWFAVWAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 MEIFITGLLLGASLLLSIGPQNVIVIXQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 MEIFVIGELEGASELLAIGPONVEVIKOGIKREGITAVIIVCELSDVVLFTEGTEGVGII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 AGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAFAASLVWFPLVGYGAAALSRPLSSPRVWRWINIGVAVVLTGLAVKLILMG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A heat-resistant lysin biosynthetic system enzyme gene of a high temperature-resistant coryneform microbe.
                                                                                                                                                                           Corynebacterium thermoaminogenes lysin biosynthetic enzyme lysE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.6%; Score 864.5; DB 4; Length 231; 71.2%; Pred. No. 1.4e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                  Heat-resistant; lysin biosynthesis; enzyme; coryneform;
aspartate-semialdehyde dehydrogenase; lysE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Mismatches
                                                     AAG64047 standard; protein; 231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR58214 standard; protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 24; 27pp; Japanese.
                                                                                                                                                                                                                                                                             Corynebacterium thermoaminogenes
                                                                                                                                                                                                                                                                                                                                                                                                    99JP-00311148
                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-00311148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 71.2%
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-364760/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAH45375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysE24 protein.
                                                                                                                                   11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2003
11-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                              08-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR58214;
                                                                                             AAG64047;
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Query Match

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RESULT 8

ABR5821

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Gaps

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Danchin A;

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carry a gene-containing vector are used to select compounds that andulate, regulate, induce or inhibit expression of the genes in plants, animals or microaganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. luminescens. Cells transformed to express the genes are useful for combinant production of the proteins, particularly toxins and antibiotical suseful as insectloides, bactericides and fungicides. The carbonisms vectors containing the genes and Ab are also useful care sensitive to P. luminescens encoded toxins or antibiotics) and as biopesticides of the genes and the proteins are as virulence care sensitive to P. luminescens encoded toxins or antibiotics) and as biopesticides of containing tragets of human diseases for which P. carons and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 AIDIRNRVRVEVSVDKQRVWVXPMLMAIVLIWLNPNAYLDAFVFIGGVGAQYGDTGRWIF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 NNSVKNRWRV------VAIIFAVTWLNPHYYLDTIVVLGSIGGQLSSDLRPWF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 LSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAV 122
                                                                                                                                                                                                                                                                                The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 IMELETTGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDL
                                                                                                                                                                 Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
                                                                                                                                                                                        useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 AAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frangeul L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 298; DB 6;
Pred. No. 1.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38; Mismatches
                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 1936; 1205pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acinetobacter baumannii protein #1611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą.
                                              Glaser P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA34450 standard; protein; 211
(CNRS ) CNRS CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 30.34
                                                Taourit S,
                                                                                                                   WPI; 2003-148459/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2003
                                              Duchaud E,
                                                                       Buchrieser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA34450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA34450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 RNRVRVEVSVDKQRVWVKPMLMAIVLTWENPNAYEDAFVFIGGVGAQYG-DTGRWIFAAG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ASAEVMKQGRW-KIIATMLAVTWLNPHVYLDTFVVLGSLGGQLDVEPKRW-FALG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDT 126
                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the YggA amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increase acidemulation of amino acids in the cell. In this case, an increase in arginine, glutamic acid and lysine is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is B. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 FITGLILGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.4%; Score 350; DB 3; Length 211; 35.7%; Pred. No. 1.6e-31; ive 37; Mismatches 75; Indels 34; Gaps
                                                                                                                      Zakataeva NP, Nakanishi K, Aleshin VV, Troshin PV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 AFAASLIWFPLVGFGAALSRPLSSPKVWRWINVVVAVWTALAIKL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 TISASFLWFFGLALLAAWLAPRLRTAKAORIINLVVGCVWWFIALQL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Photorhabdus luminescens protein seguence #1936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPWLLALVTWGGVAFLLWYGFGAFKTAMSSNIEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM68839 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 25; 29pp; English.
     99RU-00124016.
99RU-00104431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 35.7%
hes 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Photorhabdus luminescens.
                                                                          (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                2000-414802/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 211 AA;
                                                                                                                                                                                                                          N-PSDB; AAA52691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           whooping cough.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200294867-A2.
                                                                                                                                                    rokhmakova IL;
  30-DEC-1998;
09-MAR-1999;
                                                                                                                           Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2003
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67

Query Match

Best Loc Matches

ð a ð qq ₽ 셤 à g

protein.

66

ABM68839

2

Gaps

32;

Length 208; 93; Indels 62 9 101

Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;

Acinetobacter baumannii. plant biocontrol agent.

)7-FEB-2002; 2002WO-IB003040.

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07-FEB-2001; 2001FR-00001659.

(INSP) INST PASTEUR.

US6562958-B1.

04-JUN-1999; 09-JUN-1998;

Breton G,

plants

13-MAY-2003.

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The present sequence shows a Helicobacter pylori surface membrane protein, having five transmembrane regions. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of a computer evaluation. To identify likely H. pylori antignes for wascine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane controlled to particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in B. coli hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 AAPIVLDI-MRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVAT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .25 DTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 LPQTFKKKQVQTPKKLSLKKTLLFTLGVTLLNPQVYLEMVFLIGASAMSFNLVQKFVFLA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 IFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VPÍEGFGLAISLCAAVGAQSLFIVERGMARNYVFLICALCFMCDIVLMSMGVFGVGAYF- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic, vaccine, prevention, treatment, infection, envelope, identification; binding compound, bacterium, life cycle, activator, bacteria, inhibitor, duodenal ulcer disease, chronic gastritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 GAFAASLIWFPL----VGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 14.3%; Score 170.5; DB 2; Length :
l Similarity 21.5%; Pred. No. 6.5e-11;
50; Conservative 48; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 AKNLYLSLPLNLFGAVFTGFYAFLALK-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori transmembrane protein, hp2p10625orf14.
                                                                                                                                                                                                                                                                                       Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 73; Page 604; 1481pp; English.
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                               96WO-US009122.
                                                                                                95US-00487032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                       Smith D, Berglindh OT,
                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-052306/05.
N-PSDB; AAT67601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori.
                                                                                                                                                                                                                 (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 210 AA;
                               06-JUN-1996;
                                                                                                    07-JUN-1995;
                                                                                                                                       01-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
AAW20968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 AFYAAFKTNQGMELDSSQKQTLTQALITCLAFTWLNPHVXLDTIVLIGSVATQLED--KI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVIMEIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GAK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | | |: | |: | | |: | |: | | |: | |: | | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.0%; Score 298; DB 6; Length 211; 27.4%; Pred. No. 1.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H. pylori surface membrane protein 33986087.aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; SEQ ID NO 5737; 328pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW20426 standard; protein; 210 AA.
                                                                                                                                                                                                                                                (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                      98US-0088701P
                                                                                                99US-00328352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-576092/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       baumannii protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADA30324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 211 AA;
                                                                                                                                                                                                                                                                                                                         Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9640893-A1
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Query Match

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14-JUL-1997

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AAW20426;

RESULT 12 AAW2042 19-DEC-1996.

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Scarselli M;
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                                                                                       27-MAR-2002; 2002WO-IB002637
                                                                                                                 27-MAR-2001; 2001GB-00007661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Conservative
                                                                                                                                                                                                                                                              S. aureus, e.g. sepsis.
            Staphylococcus aureus.
                                                                                                                                                                   Masignani V, Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                             WPI; 2003-120786/11.
                                                                                                                                          CHIR-) CHIRON SPA
                                                                                                                                                                                                         N-PSDB; ACF73766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          whooping cough.
                                   WO200294868-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-2003
                                                            28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABM67507;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                This sequence represents a H. pylori protein likely to contain five membrane spanning regions. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 DTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPQTFKKKQVQTPKKLSLKKTLLFTLGVTLLNPQVYLEMVFLJGASAMSFNLVQKFVFLA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAPIVLDI-MRWGGIAYLLWPAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVAT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                 homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 IFITGLILGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSN 65
                                                                                                                                                                                                                       Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.3%; Score 170.5; DB 2; Length 215; 21.5%; Pred. No. 6.7e-11; Indels 43; Gaps tive 48; Mismatches 92; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GILSAAPSWILLICTMSIRYG----SKILMNQKIFMGVNIFVTAIMGTLSVIL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 GAFAASLIWFPL----VGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 AKNLYLSLFINLFGAVFTGFYAFLALK-----
                                                                                                                                                        Mellgaerd BL;
                                                                                                                                                                                                                                                                            Claim 73; Page 1359; 1481pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus protein #1446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM72206 standard; protein; 205 AA
                                                                                       95US-00487032.
                                                               96WO-US009122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 21.59
tes 50; Conservative
                                                                                                                                                      Berglindh OT,
                                                                                                                                                                                                                                                detect Helicobacter.
                                                                                                                                                                                WPI; 1997-052306/05
                                                                                                                             (ASTR ) ASTRA AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 215 AA;
                                                                                                                                                                                           N-PSDB; AAT68221
                                                                                       07-JUN-1995;
01-APR-1996;
            WO9640893-A1
                                                              06-JUN-1996;
                                      19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
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                                                                                                                                                      Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 NAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVAT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 DIRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 DGETQIMSP------MKQVSFALSVSLLNPHAILDTIGVIGSSAALYSGSNKIAFTI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 ITGLLLGASLILLSIGPQNVLVIKQGI----KREGLIAVLLVCLISDVFLFIAGTLGVDLLS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 HGFILAIGLILPLGAQNVFIFNQGANQPKYRYULPAIITAGLSDSLLIIAVVGVSIII 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TIWHDKP----ST 97
New Staphylococcus aureus protein, useful as a vaccine for treating or
preventing Staphylococcal infection, specifically an infection caused by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
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21.4%; Pred. No. 3.5e-10;
tive 47; Mismatches 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the novel S. aureus proteins of the invention
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                                                                                                                                                                                  Claim 1; SEQ ID NO 2892; 49pp; English.
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Gaps

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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the CO pypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. Luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful therageuticides. Other uses of the genes and the proteins are sensitive to P. luminescens-encoded toxins or antibiotics) and as the sensitive to P. luminescens-encoded toxins or antibiotics and sectioned for identifying targets of human diseases for which P. C. C. Iuminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                         Danchin A;
                                                                                                                                                                                                                                                                                                                                      Taourit S, Glaser P, Frangeul L, Kunst F,
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                                                                                                                                                                                                                                                        (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                       07-FEB-2002; 2002WO-IB003040.
                                                                                                                                                                                                       07-FEB-2001; 2001FR-00001659.
Photorhabdus luminescens,
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                                                   WO200294867-A2.
                                                                                                                                                                                                                                                                                                                                Duchaud E, T.
Buchrieser C;
                                                                                                   28-NOV-2002.
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11.1%; Score 132.5; DB 6; Length 205;
1 Similarity 20.5%; Pred. No. 1.5e-06;
49; Conservative 62; Mismatches 85; Indels 43; Gaps 10; 61 DLLSNAAPIVLDIMRWGGIAYLLWFAVWAAXDAMTNKVEAPQIIEETEPTVPDDTPLGGS 120 121 AVATDTRNRVRVEVSVDKORVWVKPMLMAIVLTWLNPNA---YLDAFVFIGGVGAQYGDT 177 3 IMEIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVC-LISDVFLFIAGTL-GV 60 178 GRWIFAAGAFAASLIWFPL--VGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLML 234 Query Match Best Local Similarity Matches 49; Conserv à q à 임 ð g ò

Search completed: March 12, 2004, 18:24:47 Job time : 63 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-128-152-5737
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20747 Sequence 20747, A Sequence 12661, A Sequence 1, Appli 23258 Sequence 31358, A Sequence 31358, A Sequence 6411, Appli 2552 Sequence 5121, Appli 2603 Sequence 5121, Appli 2603 Sequence 6031, Appli 2603 Sequence 6031, Appli 2603 Sequence 1608, Appli 2603 Sequence 1608, Appli 2603 Sequence 1933, A Sequence 1933, A Sequence 1933, A Sequence 1933, A Sequence 1159, Appli 2529 Sequence 7159, Appli 2529 Sequence 7159, Appli 2529 Sequence 7159, Appli 2529 Sequence 7159, Appli 2529 Sequence 7159, Appli 2529 Sequence 7159, Appli 2529 Sequence 7159, Appli 2775 Sequence 7175, Appli 2775	ALIGNMENTS 45, Application US/09489039A 46, Application US/09489039A 46, Application US/09489039A 46, Application US/09489039A 40 AND THERAPEUTICS 40 AND THERAPEUTICS 41 AND AND ANINO ACID SEQUENCES RELATING TO KLEBSIELLA VERNICON: PREMONIAE FOR DIAGNOSTICS AND THERAPEUTICS 41 AND AND AND AND ANINO ACID SEQUENCES RELATING TO KLEBSIELLA VERNICON: PROPOSITIOS AND THERAPEUTICS 42 ANINO NUMBER: US/09/489, 039A 43 ANINO DATE: 1999-01-29 44 ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO ANINO	cation US/09252991A Rubenfield et al. NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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988 88 88 99 90 90 90 90 90 90 90 90 90 90 90 90	SULT 109-489-039A-11845 Patent No. 661836 GENERAL INFORMATION: PATENT GATY BET TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITL	2-991A-24479 Se 24479, Ap. No. 6551795 INFORMATIC DATT: MARC OF INVENTIC OF INVENTIC
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Sequence 4767, Application US/09543681A

Facent No. 6605709

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
                                                                                                                                                                                    APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BUDMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBYCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.0%; Score 298; DB 4; Length 211 Best Local Similarity 27.4%; Pred. No. 8.9e-27; Matches 64; Conservative 51; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 11.6%; Score 138.5; DB 4;
Local Similarity 22.2%; Pred. No. 4.3e-08;
hes 53; Conservative 48; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 AEIMTASPILITVAKYLGATFLFVY-----
                                                                                                    Sequence 5737, Application US/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Acinetobacter baumannii
US-09-328-352-5737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                             GENERAL INFORMATION:
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US-09-543-681A-4767
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                                                            RESULT 4
US-09-328-352-5737
                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 5737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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Matches
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GENERAL INFORMATION:

APPLICANT: GARY BRETON:

TITLE OF INVENTION: ULAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-1002-001

CURRENT APPLICATION NUMBER: US(09/43,681A

CURRENT FILING DATE: 2000-04-05

PRIOR PEPLICATION WIMBER: US 60/128,706

PRIOR PEPLICATION WIMBER: US 60/128,706

NUMBER OF SEQ ID NOS: 8344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 APIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIBETEPTVPDDTPLGGSAVATDT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 LSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVBAPQIIEETEPTVPDDTPLGGSAV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 ATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 NPTILIAIARWGGIAFIJWYGLKALLRALR -----PDAL---GNAAETGP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 IMBIFITGLILGASLILSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 RNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 AAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 TFGÄVFÄSISWFFALSLLÄÄWFSPILSQVTAQRIINLFVGCVWWFIÄLQLAAQG 209
                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 FAASLIWFPLVGFGAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 26.0%; Score 310; DB 4; Length 214; Best Local Similarity 32.1%; Pred. No. 3.6e-28; Matches 75; Conservative 37; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                        Query Match 27.9%; Score 332; DB 4; Length 232; Best Local Similarity 33.5%; Pred. No. 1.1e-30; Matches 77; Conservative 42; Mismatches 77; Indels
GURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRICA APPLICATION NUMBER: US 60/074,788
FRICK FILING DATE: 1998-02-18
FRICK FILING DATE: 1998-07-27
FRICK FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Proteus mirabilis US-09-543-681A-4972
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US-09-543-681A-4972
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PACENT OF A PAPILICATION US/09134001C

PACENT NO. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: US/09/134,001C

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/065,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                60 VDLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGG 119
                                                                                                                                                                                                                                                           ----PNAAPIFN 126
                                                                                                                                                                                                                                                                                                         120 SAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPN-----AYLDAFVF--IGGVG 171
                                                                                                                                                                                                                                                                                                                                                127 VK------DLAVDSP---LKLFLMGFLTNLLNPKIAIMYLSLLPQFIHPQQGSIL 172
                                                                                                                                                                                                                                                                                                                                                                                                   172 AQYGDTGR-WIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVW----RWINVVVAVVMT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 EAPQIIEETEPTVPDDTPL/GGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 AYLDAFVFIGGVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWIN 218
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                                                                                                                                               39 IAVILVCLISDVFLFIAGTIGVDLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EKPSNIERIEP-----ILFALSVSLLNPH
                        Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 10.0%; Score 119.5; DB 4; Length 173;
1 Similarity 23.0%; Pred. No. 5.3e-06;
46; Conservative 32; Mismatches 83; Indels 39
                             DB 4;
                     10.2%; Score 121.5; DB 4
23.0%; Pred. No. 4.8e-06;
iive 41; Mismatches 89
                                                                                                                                                                                                                                                           87 ITALVVAVPYAYDTIRIAGAMYLLWLAWKALR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-328-352-6471
; Sequence 6471, Application US/09328352
; Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 VV--VAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 KVSSVIVIIVGLIÍLKNIVG 170
                   Query Match
Best Local Similarity 23.0%
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||::::|
224 GLAVRILL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 ALAIKUML 234
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Matches 46; Conserv
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Batent No. 6562958

GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION VUMBER: US/09/328,352

CURRENT APPLICATION VUMBER: US/09/328,352

WUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 IGGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGG-VGAQYG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------PWLRGVATNLFNPKALVLFIALLGSLIPAOMS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 DIGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWR---WINVVVAVVMTALAIKL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 VATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGV----GAQYGDT 177
                          106 LTGVSLLLSRTPVLFALLQALGALYLAWIGVGALRAWIRRGDGQPGRLDGALP----PSP 161
                                                                                          178 GRWIFPAGAFAASLIWFPLVGFGAA---ALSRPLSSPKVWRWINVVVAVVWTALAIKLM 233
                                                                                                                       4 MEIFITGLLCASLLLSIGPONVLVIKQGI---KREGLIAVL-LVCLISDVFLFIAGTL- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.4%; Score 135.5; DB 4; Length 260; 23.7%; Pred. No. 1.3e-07; Live 36; Mismatches 99; Indels 49; Gaps
                                                                                                                                                                                                                                                      Sequence 25992, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEGANISM: Acinetobacter baumannii
US-09-328-352-8249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                  US-09-252-991A-25992
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US-09-328-352-8249
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Sequence 18746, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: 108/09/489,039A
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
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Best Local Similarity 25.4%; Pred. No. 1.2e-05;
Matches 64; Conservative 31; Mismatches 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 RRLGVLGGAA-----
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US-09-252-991A-18746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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SEQ ID NO 7731
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APPLICANT: Gary Bre
                                                                                           RESULT 11
US-09-252-991A-18746
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LENGTH: 206
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Patent No. 6605709
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709-1002-004-05
FILE REPERENCE: 2709-1002-04-05
FRICH TILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUDANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUDANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 AAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATD 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 TRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRW----- 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.0%; Score 119.5; DB 4; Length 222; 23.1%; Pred. No. 7.7e-06;
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Matches 52; Conservative
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US-09-543-681A-4487
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US-09-328-352-6471
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BADANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTOS9-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-66-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 GSAPVVPHADR-----RALLRGLLTNLLNPKALLFCSVLLPQFVSPGAGSLAVQFAALGT 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 LLLGASLLLSIGPONVLVIKOGI---KREGLIAVLLVCLISDVFLFIAGTLGVDLLSNAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 LIALAVVYLVPGPDMLLLFQTGARQGRRAALVTALGLALARACHVLMAAT-GLALLFRTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 ------GDTGRWIFAAGAFAASLIW---FPLVGFGA-AALSRPL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 VLVLVGLAFDCAYALAGGRLGRWLASRPRAQRLQQWGFGGLLIGFGVRLALLRQL 222
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 --LIWLTVLAWKLYNYN----PVISLEKNEQYP---PIGFKA---
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.3%; Score 111; DB 4; Best Local Similarity 2.4%; Pred. No. 7.6e-05; Marches 93; Conservative 27; Mismatches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26644
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Patent No. 6562958
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                     US-09-252-991A-26644
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Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION:
DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
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TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
THERAPERANCE: 2709-1002-001
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                 116
                                                                                                                                                                                                     117 LGGSAVAIDIRNRVRVEVSVDKORVWVKPMLMAIVLIWLNPNAYLDAFVFIGGVGAQYGD 176
                                                                                                                                                                                                                                                                                                                                             64 SNAAPIVLDIMRWGGIAYLLWFAV-----MAAKDAMTNKVEAPQIIEETEPTVPDDTP 116
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                                                                            17 YLTYLVGAVFIILVPGPNTFFVLKTGIAHGVKKGYLAAAGV-FIGDAVLMFLAFAGVATL 75
                             63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 FITGLLIGASLLLSIGPONVLVIKOGIKR---EGLLAVLLVCLISDVFLFIAGTLGVDLL
                     7 FITGLLLGASLLLSIGPONVLVIKQGIK---REGLIAVLLVCLISDVFLFIAGTLGVDLL
                                                                                                                                                                 ---FAVMAAKDAMTN-KVEAPQIIEETEPTVPDDTP
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CURRENT APPLICATION NUMBER: US/09/252,991A
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                                                                                                                                                                                                                                                                                                                                                                                                                                            177 TGRWIFAAGAFAASLIWFPLVGFGA 201
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GENERAL INFORMATION:
                                                                                                                                                             64 SNAAPIVLDIMRWGGIAYLLW--
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Best Local Similarity 23.1%;
Matches 56; Conservative 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Proteus mirabilis
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US-09-543-681A-4854
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GenCore version 5.1.6

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OM protein - protein search, using sw model

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March 18, 2004, 06:36:47; Search time 43 Seconds

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1421.243 Million cell updates/sec

Title:

US-09-105-117K-2

Perfect score: 1191

I WVINNEFITGLLLGASILLS......INVVAVVMTALAIKIMUMG 236

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1049977 seqs, 258955339 residues
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Published Applications AA:*

1: \(\text{cgn2} = \tilde{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{TPBCOMB} \). pep:*

2: \(\text{cgn2} = \tilde{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{TMF} \) PUB. \(\text{Pup} \); \(\text{cgn2} = \tilde{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{TMF} \) PUB. \(\text{Pup} \); \(\text{cgn2} = \tilde{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{TMF} \) PUB. \(\text{Pup} \); \(\text{cgn2} = \tilde{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{TMF} \) PUB. \(\text{Pup} \); \(\text{cgn2} = \tilde{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{TMF} \) PUB. \(\text{Pup} \); \(\text{cgn2} = \tilde{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{TMF} \) PUB. \(\text{Pup} \); \(\text{cgn2} = \tilde{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{PuBCOMB} \), \(\text{Pup} \); \(\text{cgn2} = \tilde{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{PuBCOMB} \), \(\text{Pup} \); \(\text{cgn2} = \text{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{PuBCOMB} \), \(\text{Pup} \); \(\text{cgn2} = \text{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{PuBCOMB} \), \(\text{Pup} \); \(\text{cgn2} = \text{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{PuBCOMB} \), \(\text{Pup} \); \(\text{cgn2} = \text{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{PuBCOMB} \), \(\text{Pup} \); \(\text{cgn2} = \text{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{PuBCOMB} \), \(\text{Pup} \); \(\text{cgn2} = \text{6} \text{ptodata} / 2 \text{pubpaa} / USO \(\text{PuBCOMB} \), \(\text{Pup} \); \(\text{Pup} \); \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\text{Pup} \), \(\te

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

99999 888 88 89990 81111	88 7.4	88 7.4 460	88 7.4 460	7.4	7.4	7.4	7.4	7.4	.5 7.4	.5 7.4	7.5	7.5	7.5	7.5	7.6	7.6		7.6	91 7.6	91 7.6	7.6	9.7	7.6	7.7	7.7	7.7	· · ·		7.7	7.7
888 8990	88 7	88 7	88 7	88 7	88 7	88 7	88 7	88 7		88.5 7	89 7	89.5	89.5	89.5	90.5	91 7	1 :	91 7	91 7	91 7	91 7	91 7	91 7				91.5 7	91.5 7	92.5 7	
18	118 92 93 7 8 92 93 7 9 93 93 93 93 93 93 93 93 93 93 93 93 9	93 93 93 93 93 93 93 93 93 93 93 93 93 9	93 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 91.5 7.7 91.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91	93 93 93 93 93 93 93 93 93 93 93 93 93 9	93 7.8 91.5 7.7 9 91.5 9.7 9 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91	93 7.8 9.1.5 7.7 9.1.5 7.7 9.1.5 7.7 9.1.5 7.7 9.1.5 7.7 9.1.5 7.7 9.1.5 7.7 9.1.5 7.7 9.1.5 7.7 9.1.5 7.7 9.1.5 7.7 9.1.5 7.5 9.1.5 7.5 9.1.5 7.5 9.1.5 7.5 9.1.5 7.5 9.1.5 7.5 9.1.5 7.5 9.1.5 9.1.5 7.5 9.1.5 9.1.5 7.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 9.1.5 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7.7 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.7 91 7.6 91 7.7 91 7.6	93 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.6 91 7.	93 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6 90.5 7.5 90.5 7.5	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6 91 7.6 91 7.6	93 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6 91 7.6	93. 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6	93 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6	93 93 94 95 95 95 95 95 95 95 95 95 95 95 95 95	92 93 92.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7	7.8 7.8 7.7	7.8	7.8	
17 18 92	88888888888888888888888888888888888888	93 7.8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	93 7.8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	93 93 91.5 7.7 8 91.5 7.7 9 91.5 7.7 9 91.5 7.7 9 91.5 7.7 7 91.5 7.7 7 91.5 7.7 7 91.5 7.7 7 91.7 6 99.5 7 7 5 88 8 7 7 5 88 8 8 7 7 8 88 8 8 7 7 8 88 7 7 8 88 8 7 7 8 88 7 7 8 88 7 7 7 8 88 7 7 7 8 88 7 7 7 8 88 7 7 7 8 88 7 7 7 8 88 7 7 8 8 88 7 7 8 8 88 7 7 8 8 88 7 7 8 8 88 7 7 8 8 88 7 7 8 8 88 7 7 8 8 88 7 7 8 8 88 7 7 8 8 8 88 7 7 8 8 8 88 7 7 8 8 8 8	93 7.8 93 7.8 93 7.8 93 7.5 94 95 95 95 95 95 95 95 95 95 95 95 95 95	93 7.8 93 7.8 91.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 91.5 7.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91	93 7.8 93.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 91.5 7.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91	93 7.8 92.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91	93 7.8 93 7.8 91.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91	93 7.8 93 7.8 91.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 7.5 91.5 91.5 7.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6 90.5 7.5 89.5 7.5	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.6 91.5 7.6 91.5 7.6 91.5 7.6 91.5 7.6 91.5 7.6 91.5 7.6 91.5 7.6 91.7 61.5 7.5 91.7 61.5 7.5 91.7 61.5 91.7 61.5 91.7 61.5 91.7 61.5 91.7 61.5 91.7 61.5 91.7 61.5 91.7 61.5 91.7 61.5 91.7 61.5 91.7 61.5 91.7 61.5 91.5 7.5 91.7 61.5 91.5 7.5 91.7 61.5 91.5 7.5 91.7 61.5 91.5 7.5 91.7 61.5 91.5 7.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6 90.5 7.5	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6 91 7.6 91 7.6	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6 91 7.6	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7 91 7.6 91 7.6	93 92 91.5 91.5 91.5 91	93 92.5 91.5 91.5 91.5	93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7 91.5 7.7	93 7.8 93 7.8 92.5 7.8 91.5 7.7 91.5 7.7 91.5 7.7	93 7.8 93 7.8 92.5 7.8 91.5 7.7 91.5 7.7	93 7.8 92.53 7.8 91.5 7.7 91.5 7.7	93 7.8 93 7.8 92.5 7.8 91.5 7.7 91.5 7.7	93 7.8 93 7.8 92.5 7.8 91.5 7.7	7.8 7.8 7.7	7.8 7.8	7.8	3 7.8

ALIGNMENTS

US-09-738-626-6955
; Sequence 6955. Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: MAXGAGMAM, SATOSHI
APPLICANT: MAXGAGMAM, SATOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: TATESHIN, MIXERO
APPLICANT: TATESHIN, MAXEO
APPLICANT: TATESHIN, NAXEO
APPLICANT: TATESHIN, NAXEO
APPLICANT: TATESHIN, NAXEO
APPLICANT: TATESHIN, NAXEO
APPLICANT: TEXDA, MASATO
APPLICANT: SENOH, AKHINO
APPLICANT: SENOH, AKHINO
APPLICANT: SENOH, AKHINO
APPLICANT: SENOH, AKHINO
APPLICANT: SENOH, AKHINO
FILER REFERENCE: 249-125
CURRENT APPLICATION UNDER: US/09/738, 626
CURRENT APPLICATION UNDER: UP 99/377484
; PRIOR PLICATION UNDER: JP 90/159162
; PRIOR PELICATION NUMBER: JP 90/159162
; PRIOR PELICATION NUMBER: JP 00/280988
; PRIOR PLING DATE: 2000-04-07
; PRIOR PLING DATE: 2000-04-07
; PRIOR PLING DATE: 2000-04-07
; PRIOR PLING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7659
; SOOTWARE: PRI
TYPE: PRI
TYPE: PRI
US-09-738-626-6955

Ouery Match
100.0%; Score 1191; DB 9; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.1e-117;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps

; 0

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121 IDTRNRVRVEVSVDKQRVWVKPMLMAIULTWINPNAYLDAFVPIGGVGAQYGDTGRWIFA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SNAAPIVLDIMRWGGIAYILWFAVWAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVBAPQIIEBTEPTVPDDTPLGGSAVA 123
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APPLICANT: TIO, HISAO
APPLICANT: TIO, HISAO
APPLICANT: TOO, HISAO
APPLICANT: YASHINA
APPLICANT: YASHINA
TITLE OF INVENTION: METHOD FOR PRODUCING L-ARGININE
FILE REPREMENCE: 223391USO
CURRENT APPLICATION NUMBER: US/10/196,232
CURRENT PILING DATE: 2002-07-17
PRIOR FILING DATE: 2001-07-25
NUMBER: PRIOR APPLICATION NUMBER: 107-25
NUMBER: PRIOR PRIOR DATE: 2001-07-25
NUMBER: PRIOR PRIOR DATE: 2001-07-25
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NUMBER: PRIOR DATE: 2001-07-25
NUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.9%; Score 1178; DB 14; Best Local Similarity 100.0%; Pred. No. 1.4e-115; Matches 233; Conservative 0; Mismatches 0;
        METABOLIC PATHWAY PROTEINS
                          FILE OF INVENTION: METABOLIC PATHWAI PROJECT INTER OF INVENTION NUMBER: US/09/746,660A CURRENT PLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/746,660A PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR PRIOR PRIORITION NUMBER: 60/14613
PRIOR FILING DATE: 1999-07-02
PRIOR PRIOR OF THE SOUND PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIO
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SEQ ID NO 52
LENGTH: 233
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US-10-196-232-25
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APPLICANT: WASHEDA, HISASHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL
TITLE OF INVENTION: ASSIMILATING BACTERIUM
FILE REFERENCE: 223789US
CURRENT APPLICATION NUMBER: US/10/166,142
CURRENT PILING DATE: 2002-06-11
PRIOR PILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
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1 MVIMEIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGV
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Publication No. US20030049804A1
GENERAL INFORMATION:
APPLICANT: Pompel, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Abricant: Applicant: Applicant: Haberhauer, Osear
APPLICANT: Lee, Heung-Schick
APPLICANT: Lee, Heung-Schick
APPLICANT: Lee, Heung-Schick
APPLICANT: Haberhauer, Gregor
APPLICANT: Hew Heung, Byung-Joon
APPLICANT: Hew Heung, Byung-Joon
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
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Publication No. US20030124687A1
GENERAL INFORMATION:
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Best Local Similarity 100.'
Matches 236; Conservative
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US-09-746-660A-52
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US-10-166-142-8
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                                                                                                                                                                                      25.3%; Score 301; DB 14; Length 203; 32.1%; Pred. No. 2.3e-23; ive 32; Mismatches 86; Indels 3
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APPLICANT: HATTORI, MASAHIRA
ITITLE OF INVENTIORI, NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-56.
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: JP 2001-272697
FRIOR FILING DATE: 2001-05-30
FRIOR APPLICATION NUMBER: JP 2001-272697
FRIOR APPLICATION NUMBER: JP 2001-272697
FRIOR APPLICATION NUMBER: JP 2001-272697
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FRIOR APPLICATION NUMBER: JP 2001-272697
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                                                                                  ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8659
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
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Best Local Similarity 24.2*
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8659
LENGTH: 203
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Matches 72; Conservative
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APPLICANT: GUNCI, YOSHIYA
APPLICANT: YASUEDA, HISASHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL
TITLE OF INVENTION: ASSIMILATING BACTERIUM
FILE REFERENCE: 223781LATING BACTERIUM
FILE REFERENCE: 223781LATING BACTERIUM
CURRENT APPLICATION NUMBER: US/10/166,142
PRIOR APPLICATION NUMBER: US/201-1777075
PRIOR FILING DATE: 2002-06-11
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
                                                                                                                                                                       61 SNAAPIVLDIMRWGGIAYLLWFAVWAAKDAMTNKVBAPQIIEETEPTVPDDTPLGGSAVA 120
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                                                                                                                                64 SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVA 123
                                                                                                                                                                                                                                      124 IDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFA 183
                                                                    1 MEIFITGLLLGASLLLSIGPQNVLVIKQSIKRBGLIAVLVCLISDVFLFIAGTLGVDLL 60
                         MEIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL 63
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                                                                                                                                                                                                                                                                                                                                               184 AGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                    49.0%; Score 584; DB 14; Length 124; 100.0%; Pred. No. 2e-53; cive 0; Mismatches 0; Indels
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAVOSHI
APPLICANT: SHIBA, TADAVOSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPRENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR PRIOR DATE: 2001-05-31
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Matches 118; Conservative
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117 LGGSAVAIDIRNRVRVEVSVDKQRVWVKPMLMAIVLIWLNPNAYLDAFVFIGGVGAQYGD 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 TGR----WIFAAGAFAA-----SLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 AGAPKLPVÍTÁLAÁPÓALFEVGYYGMYVWÉ-----VGRMKKVÍSRAGVRRALEQVSGGV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                           59 ALGLTALLAASRTAYDVWRIGGAVVLVWYGVQTLRAARRG------EARPSAADD-- 107
                                                                                                                                                                                                                                                                                      4 MEIFITGLL--LGASLLLSI--GPQNVLVIXQGI--KREGLIAVLLVCLISDVFLF-IAG 56
                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA,034A
                                                                                                                                                                                                                                                                                                                                                                                               57 ILGVDLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTP
                                                                                                                                                                             10.8%; Score 128.5; DB 12; Length 212; 25.0%; Pred, No. 3.5e-05; tive 34; Mismatches 93; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PLILOR DATE: 2000-05-26
PRIOR PLILOR DATE: 2000-09-06
PRIOR PLILOR DATE: 2000-09-06
PRIOR PLILOR DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PLILORION NUMBER: 60/253,625
PRIOR PLILORION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR PLILOR DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PLILOR DATE: 2000-11-27
PRIOR PLILOR DATE: 2000-11-27
PRIOR PLILOR DATE: 2000-11-27
PRIOR PLILOR DATE: 2000-12-22
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; Sequence 77618, Application US/10282122A
; Publication No. US20040029129A1
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                      ; ORGANISM: Streptomyces cattleya US-10-374-903A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Wall, Daniel
Trawick, John
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                    62; Conservative
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 6
LENGTH: 212
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201 LVLLGIRM 208
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Best Local Similarity
Matches 62; Conserv
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 DTRNRVRVBVSVDKQRVWVKPMLMAIVLTWL-NPNAYLDAFVFIGGVGAQY--GDTG-RW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 IFAAGAF--AASLIWFPLVGFGAAALSRPLSS--PKVWRWINVVVAVVMTALAIKLMLMG 236
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        150 LSILPQFVHGGGSTSRQIFFLGTLDIVIGVAYWFALVAV-AARLRAFLARPKVRHGWELT 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.1%; Score 132.5; DB 9; Length 226; Best Local Similarity 24.2%; Pred. No. 1.5e-05; Matches 58; Conservative 45; Mismatches 98; Indels 39; Gaps
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APPLICANT: University of Oviedo
APPLICANT: Astur Pharma, S.A.
TITLE OF INVENTION: The gene cluster for thienamycin biosynthesis,
TITLE OF INVENTION: genetic manipulation and utility
CHRENT APPLICATION NUMBER: US/10/374,903A
CURRENT FILING DATE: 2003-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER: OF SEQ 1D NOS: 7059
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PRIOR APPLICATION NUMBER: JP 99/377484
                                                                                                                                                                                                                                       Sequence 3665, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3665
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                                                         216 --WINVVVAVVMTALA 229
                                                                                          | : : : | |
209 TGWLFIAIGIGVAAAA 224
                                                                                                                                                                                                                                                                                                                                             MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                            HAYASHI, MIKIRO OCHIAI, KEIKO YOKOI, HARUHIKO TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin ver. 3.0
SEQ ID NO 3665
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IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 249-125
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Foreyth, Robert
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVARIATION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/242,579
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,579
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
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PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-3
PRIOR PILING DATE: 2000-12-3
PRIOR PILING DATE: 2000-12-3
PRIOR PILING DATE: 2000-12-3
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR PILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2000-10-216
PRIOR PILING DATE: 2000-10-20-16
PRIOR PILING DATE: 2000-10-20-16
PRIOR PILING DATE: 2000-10-20-16
PRIOR PILING DATE: 2000-10-20-16
PRIOR PILING DATE: 2000-10-20-16
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PRIOR PILING DATE: 2000-10-20-16
PRIOR PILING DATE: 2000-10-20-16
PRIOR PILING DATE: 2000-10-20-16
                                                          125 DTRNRVRVEVSVDKORVWVKPMLMAIVLTWLNPNA--YLDAFVFIGGVGAQ-YGDTGRWI 181
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                                                                                                                                                                                FVLAAFVASASWQVLLAGGGALLGRALTGRRGRLVTALLSSAVILGLAVRMLM 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51;
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Publication No. US20040029129A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Yamamoto, Robert
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Zyskind, Judith
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Best Local Similarity
Matches 48; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 DIPLGGSAVAIDIRNRVRVEVSVDKQRVWVKPMLMAIVLIMLNPNAYLDAFVF---- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 -----GEGA--AALSR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 FILGLVVLSVTGVEALYADMGHF----GIKPIRIAWFALVMPSILLNYFGQGAYLLTLSA 270
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                                                                                                                                                                                                                                                                                                                                                                                         2 VIMEIFITGLLIGASLLLSIGPONVLVIKOGIKREGLIA-----VLLVCLISDVFLFI 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 VAGLLAGYGIAVPVGAVATYLVSLTARTSLRTGVCAALGVATADGLYALVA-ALGGSALA 64
                                                                                                                                                                                                                                                                                                                              72; Indels 112; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.2%; Score 109.5; DB 14; Length 210; 22.7%; Pred. No. 0.0035; Live 36; Mismatches 107; Indels 37; Gaps
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1 SEQ ID NO 77618 LENGTH: 620
                                                                                                                                                                                                                                                                      10.0%; Score 119; DB 12; Length 620; 22.8%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 VQAMGTERIGRFFAPVM------LLWFLVLAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 PIGSTFFSLAPKAWLWPLILLATFATVIASQAVISG 306
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                                                                                                                                                                                                                                                                                                                                 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTOKI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILLING DATE: 2002-05-29
FRICH APPLICATION NUMBER: US 2001-204089
PRICH FILING DATE: 2001-05-30
PRICH FILING DATE: 2001-05-30
PRICH FILING DATE: 2001-05-30
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PRICH FILING DATE: 2001-08-30
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Publication No. US2030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: INEDA, HARUO
APPLICANT: ISHIKAMA, JUN
APPLICANT: HORIKAMA, HINOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Streptomyces avermitilis US-10-156-761-14994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.2% Best Local Similarity 22.7% Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 ---LGAHA----
                                                                                                                                                                                                                                                                                                                                 63; Conservative
                                                                                                                                                                                ; ORGANISM: Vibrio cholerae
US-10-282-122A-77618
                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-10-156-761-14994
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APPLICANT: Yamanolo, Koderc
APPLICANT: Yamanolo, Koderc
APPLICANT: Yamanolo, Koderc
APPLICANT: Yau, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 05/10/26,2122A
CURRENT PILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
FRIOR PAPLICATION NUMBER: 60/207,727
FRIOR FILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: 60/230,335
FRIOR APPLICATION NUMBER: 60/230,335
FRIOR PAPLICATION NUMBER: 60/230,335
FRIOR PELING DATE: 2000-09-06
FRIOR PILING DATE: 2000-09-06
FRIOR PILING DATE: 2000-10-23
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FRIOR PELING DATE: 2000-11-27
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FRIOR APPLICATION NUMBER: 60/269,308
FRIOR PELING DATE: 2001-02-16
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR PELING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 VGA------QYGDTGRWIFAAGAFAASLIWFPL-VGFGAAALSRPLSSPKVWR 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 -----SRLPLLIYGVALGGMNFLFYMSL-------KTVP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.0%; Score 95; DB 1
Best Local Similarity 24.2%; Pred. No. 0.18;
Matches 63; Conservative 42; Mismatches
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 WINVVVAVVMTALAIKLMLM 235
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212 -IALAVAILSTALPYSLEMV 230
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US-10-282-122A-77782
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--AIVFLLAVLPQFLDLSKPQWIQYL-IMAATWVTIDLIVMAGYTGLASKVLRLLRSPKQ 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 FITGLLLGASLLLSIGPQNVLVI----KQGIKREGLIAVLLVCLISDVFLFIAGTLGVDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 ILQANALLFGIVKYAGAGYLTWLAFGMLRAAWEMWRTRRDRADAARAVV---
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIRAMA, UNON
APPLICANT: HORIKAMA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: BALTOKI, MASANIRA
TITLE OF INVENTION: MAUNER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FLILING DATE: 2010-05-30
PRIOR FLILING DATE: 2010-05-30
PRIOR FLILING DATE: 2010-05-30
PRIOR FLILING DATE: 2010-06-30
PRIOR FLILING DATE: 2010-06-30
PRIOR FLILING DATE: 2010-06-30
PRIOR FLILING DATE: 2010-06-30
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                                                                                                                                                                                                                                                                                    Sequence 10918, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-10918
                                                                                                                          156 OKYLNRGFAVMFSCAALLL 174
                                                               214 WRWINVVVAVVMTALAIKL 232
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Oylsen, Wari
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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Gaps

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95; Indels 77; Gaps 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 FVFIGGVG-------AQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 ETEPTVPDDTPLGGSAVAT-DTRNRVRVEVSVDKQ-RVWVKPMLMAIVLTWLNPNAYLDA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 LG------VDLLSNAAPIVLDIMRWGGIAY--LLWFAVM---AAKDAMTNKVEAPQIIE 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 ITGLLLG---ASLILSIGPQNVLV----IKQGIKR--EGLIAVLLVCLISDVFLFIAGT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.9%; Score 93.5; DB 9; Length 452; Best Local Similarity 19.4%; Pred. No. 0.47; Matches 52; Conservative 44; Mismatches 95; Indels 7
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in FITLE OF INVENTION: Processoryotes FILE EFFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 00/191,078
FRIOR APPLICATION NUMBER: 60/191,078
FRIOR FILING DATE: 2000-03-21
FRIOR FILING DATE: 2000-05-26
FRIOR PLICATION NUMBER: 60/207,727
FRIOR PLICATION NUMBER: 60/207,727
FRIOR PLICATION NUMBER: 60/207,727
FRIOR PLICATION NUMBER: 60/203,625
FRIOR PLICATION NUMBER: 60/203,625
FRIOR PLICATION NUMBER: 60/203,625
FRIOR PLICATION NUMBER: 60/203,931
FRIOR FILING DATE: 2000-11-27
FRIOR PLICATION NUMBER: 60/203,931
FRIOR PLICATION NUMBER: 60/203,931
FRIOR PLICATION NUMBER: 60/203,931
FRIOR PLICATION NUMBER: 60/209,308
FRIOR PLICATION NUMBER: 60/209,308
FRIOR PLICATION NUMBER: 60/209,308
FRIOR PLICATION NUMBER: 60/209,308
FRIOR FLING DATE: 2000-10-216
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 10183
LENGTH: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 SSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 MFIPF-----VLVQPILAAAITLAAYYMG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: March 18, 2004, 06:44:48
Job time : 44 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Escherichia coli
US-09-815-242-10183
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GenCore version 5.1.6
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OM protein - protein search, using sw model

March 12, 2004, 18:20:36 ; Search time 20 Seconds
(without alignments)
1135.060 Million cell updates/sec Run on:

US-09-105-117K-2 1191 1 WVIMEIFITGLILGASLILS.....INVVVAVVMTALAIKLMLMG 236 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

283366

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	hypothetical 23K p	probable membrane	hypothetical prote	hypothetical prote	probable LysE type	probable transport	LysE family transp	probable membrane	hypothetical prote	hypothetical prote		LysE/YggA family p	YggA protein homol	conserved hypothet	conserved hypothet	hypothetical prote	conserved hypothet	uncharacterized co	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	efflux protein, Ly	hypothetical prote	efflux protein, Ly	ротаввічт uptake p	hypothetical prote	RhtB family transp	dihydrodipicolinat
CI CI	QQECSA	AH0874	B91103	E85948	AG0112	D83100	AG2690	C97472	C70744	H70756	AD3411	B82318	S57940	D69838	F64609	B71906	B89854	C97219	E97789	B69066	G83703	F83444	E87252	D84016	G87305	F82449	B83280	AH3203	G84086
DB	H	N	7	7	~	7	7	7	7	~	7	(7	7	N	7	7	7	N	7	Н	7	~1	7	7	7	~	~	7	7
Length	211	211	211	211	205	200	202	202	201	199	204	211	211	220	210	210	205	205	213	208	200	213	210	210	208	620	197	216	208
% Query Match	29.4	29.1	28.8	28.5	28.1	27.9	27.4	27.4	26.8	26.7	25.4	20.6	20.0	14.8	14.6	14.3	13.8	13.0	12.9	12.7	12.4	11.5	11.1		10.1	10.0	6.6	9.7	9.6
Score	350	347	343	340	335	332	326.5	326.5	319	318	302.5	245.5	238	176.5	173.5	170.5	164	154.5	153.5	151.5	148	136.5	132	130	120.5	119	117.5	115.5	114.5
Result No.	1	7	m	4	ιΩ	9	7	80	6	10	11	12	13	14	15	16	. 17	18	19	20	21	22	23	24	25	26	27	28	29

efflux protein, Ly	RhtB family transp	hypothetical prote	probable membrane	probable amino aci	probable hyuE APE1	RhtB family transp	conserved hypothet	branched-chain ami	hypothetical prote	threonine efflux p	hypothetical prote	iron(III) dicitrat	conserved hypothet	threonine efflux p	yfuD protein [impo
164	04	62	714	600	:615	2683	7464	H69277	1082	3223	3010	G98273	B83356	0466	43921
E872	A D29	F976	AD07	A96	E72	Ā	8	He	689	A96	AG	8	B8:	Ĕ	7
2 E87264	2 AD29	2 F976'	2 AD07	2 A96	2 E72	2 AB	2 H9	2 H6	2 683	2 A96	2 AG	2 69	2 B8	2 AH	2 T4
7	7	7	~	7	7	N	7	7	7	7	7	~	205 2 B8	~	2
7	235 2	235 2	212 2	218 2	450 2	203 2	239 2	284 2	210 2	206 2	349 2	349 2	~	206 2	212 2 7
9.5 222 2	9.5 235 2	235 2	9.3 212 2	9.2 218 2	9.2 450 2	9.1 203 2	9.1 239 2	9.0 284 2	9.0 210 2	8.8 206 2	8.8 349 2	8.8 349 2	205 2	8.6 206 2	8.6 212 2 1

ALIGNMENTS

RESULT 1
VXBC5A VXBC184 23K protein (sbm-fba intergenic region) - Escherichia coli (strain K-12) C:Species: Racherichia coli
C;Date: 31-Dec-1990 #sequence_revision 17-Oct-1997 #text_change 01-Mar-2002
C;Accession: Boso(7) 504/36 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd
.A.; Rose, D.J.; Mau, B.; Shao, Y.
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID: 9742617; PMID: 9278503
A; Accession: B65077
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A;Residues: 1-211 <blat></blat>
A; Cross-references: GB: AE000375; GB: U00096; NID: 91789282; PIDN: AAC75960.1; PID: 91789299.
A; Experimental source: strain K-12, substrain MG1655
R; Alefounder, P.R.; Perham, R.N.
Mol. Microbiol. 3, 723-732, 1989
A; Title: Identification, molecular cloning and sequence analysis of a gene cluster encod
hyde 3-phosphate dehydrogenase of Escherichia coli.
A; Reference number: S04730; MUID:89313302; PMID:2546007
A; Accession: S04736
A; Molecule type: DNA
A;Residues: 15-211 <ale></ale>
A; Cross-references: EMBL: X14436; NID: 941417; PIDN: CAA32607.1; PID: 941425
C:Genetics:

C;demetucs. A;Gene: ygg# A;Map position: 63 min C;Superfamily: Bscherichia coli hypothetical 23K protein (sbm-fba intergenic region)

34; Query Match 29.4%; Score 350; DB 1; Length 211; Best Local Similarity 35.7%; Pred. No. 1.5e-24; Matches 81; Conservative 37; Mismatches 75; Indels 3

67 APIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETBPTVPDDTPLGGSAVATDT 126 127 RNRVRVEVSVDKQRVWVKPMLMAIVLTWINPNAYLDAFVFIGGVGAQYG-DTGRWIFAAG 185 셤 ò g ò g ò

186 AFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL 232 중 음

8 6 8 6 8 6	ERSULT 4 ERSULT 4 ERSULT 4 ERSULT 4 ERSULT 4 ERSULT 4 ERSULT 4 ERSULT 4 ERSULT 4 ERSULT 4 ERSULT 4 ERSULT 4 ERSULT 4 ERSULT 4 ENDISITED 0157:H7, substrain EDL9 C;Species: Escherichia coli C;Species: Escherichia coli C;Accession: ESS948 E;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2011 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUD:21074935; PMID:11206551	A; Modecule types: DNA A; Residues: 1-211 <cr> A; Residues: 1-211 <cr> A; Residues: 1-211 <cr> A; Residues: 1-211 <cr> A; Residues: 1-211 <cr> A; Residues: 1-211 <cr> C; Genetics: A; Experimental source: strain O157:H7, substrain EDL933 C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: YegA C; Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)</cr></cr></cr></cr></cr></cr>	Query Match 28.5%; Score 340; DB 2; Length 211; Best Local Similarity 34.5%; Pred. No. 1.2e-23; Matches 78; Conservative 37; Mismatches 79; Indels 32; Gaps 2; Qy 7 FITGILLGASLILSIGPONVLVIKQGIRKEGLIAVILVCLISDVFLFIAGTLGVDLLSNA 66	Db 65 SPM_LILIVENGGVELLMYGRCAFKTAMSSNIEL	RESULT 5 AG0112 probable LysE type translocator YP00918 [imported] - Yersinia pestis (strain C092) C;Species: Yersinia pestis C;Decies: Versinia pestis C;Decies: Versinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001 C;Accession: AG0112 R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.I. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001 A;Title: Genome sequence of Yersinia pestis, the causative agent of plaque. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AG0112 A;Status: preliminary A;Rolacule type: DAA A;Residues: 1-205 cKUR> A;Residues: 1-205 cKUR> C;Genetics:
RESULT 2 AH0874 probable membrane transport protein STY3222 [imported] - Salmonella enterica subsp. ente C;Species: Salmonella enterica subsp. enterica serovar Typhi C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Bate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AH0874 R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature all, 848-852, 2001 Nature all, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov	PDB:GN0017	QY 3 IMBIFITGLIGASLLISTGPONVLVIKQGIRREGLIAVLLVCLISDVFLFIAGTLGVDL 62 1 MISYYFQGVALGAAMILPLGFQNFVINQGIRREGLIAVLLVCLISDVFLFIAGTLGVDL 62 Db 1 MISYYFQGVALGAAMILPLGFQNFVINQGIRREGLIAVLLCALSDLVLISAGIFGGSA 60 QY 63 LSNAAPIVLDIANFRAGATALMFAVMAAKDAMTNKVBAPQIIEETEPTVPDDTPLGGSAV 122 Db 61 LLMQSPWLLALVTWGGVAFLLMYGFGALKTAMSSNLEL	OY 123 ATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYG-DTGRWI 181 Db 99ASAEVMKQGRW-KIIATMLAVTWLNPHVYLDTFVVLGSLGGQLAMBPKRW- 147 QY 182 FAAGAFAASLIMPPLVGFGAAALSRPLSSPKWRWINVVVAVWYTALAIKLMLMG 236 QY 182 FAAGAFAASLIMPFLVGFGAALSRPLSSPKWRWINVVVAVWYTALAIKLMLMG 236 Db 148 FALGTISASFLWFFGLALLAAWLAPRLRTAKAQRIINILVGVVWMLIAFQLAREG 202	RESULT 3 B91103 hypothetical protein EC83794 [imported] - Escherichia coli (strain O157:H7, substra. C, Species: Escherichia coli C, Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C, Accession: B91103 R, Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunagay T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and	A;Rectence number: A99629; MUID:21156231; PMID:11258796 A;Accession: B91103 A;Status: preliminary A;Accession: B91103 A;Residues: 1-211 cHAY> A;Residues: 1-211 cHAY> A;Residues: 1-211 cHAY> A;Residues: 1-211 cHAY> A;Residues: 1-211 cHAY> A;COSS-references: GB:BA000007; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;Escidues: 1-211 cHAY> A;COSS-references: GB:BA000007; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000007; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000007; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000017; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000007; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000017; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000017; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000017; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000017; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000017; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000017; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000017; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000017; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000017; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000017; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN00154 A;COSS-references: GB:BA000017; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN0017; PIDN:BAB37217.1; PID:g13362266; GSPDB:GN0017; PIDN:BAB37217.1; PID:g1362266; GSPDB:GN0017; PIDN:BAB37217.1; PID:g136222222222222222222222222222222222222

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Diobable membrane transport protein. (AL357613) [imported] - Agrobacterium tumefaciens c) Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Accession: C97472 [S; Godner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Scince 294, 2323-2328, 2001 [Artitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID: 21608551; PMID: 11743194
LysE family transporter lysE [imported] - Agrobacterium tumefaciens (strain C58, Dupont: Species: Agrobacterium tumefaciens C.Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C.Accession: AG2690
                                                                                                                     Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Jerge, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel.; Kary, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: 1ysE
A;Map position: circular chromosome
C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map positīon: circular chromosome
C;Superfamily; Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)
                                                                                                                                                                                                                                                                                                             A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AG2690
                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-202 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41941.1; PID:g17739308; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: AE007869; PIDN: AAK86732.1; PID: 915155924; GSPDB: GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3. IQIFFTGLIMGLSLIVALGAQNAFVIKQGLARSHVFAVCATCAISDALLIMVGVFGFQRI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 MEIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 IDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 MEIFITGLLLGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 AGAATGSLLFFFSLGYGARWLRPIFEKPSAWRILEGVIAITWWAIAFKLVM 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 AGAFAASLIWFPLVGFGAALSRPLSSPKVWRWINVVVAVVWTALAIKLML 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.4%; Score 326.5; DB 2; Length 202; 31.6%; Pred. No. 2e-22; tive 42; Mismatches 83; Indels 33
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A;Molecule type: DNA
A;Residues: 1-202 <KUR>
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C;Species: Pseudomonas aeruginoāa
C;Accession: D93100
C;Accession: D93100
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Afitle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Accession: D83100
A;Accession: D83100
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: DNA
A; Residues: 1-200 <STO>
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A; Residues: 1-200 <STO>
A; Cross-references: GB:AE004852; GB:AE004091; NID:g9950587; PIDN:AAG07753.1; GSPDB:GN001
A; Experimental source: strain PAO1
C; Genetics:
A; Gene: PA4365
C; Superfamily: Escherichia coli hypothetical 23K protein (abm-fba intergenic region)
   A,Gene: YP00918
C,Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 DGVASSATSVTQGRWRILVTL------LAVTWLNPHVYLDTFVVLGSLGGQLL 141
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                                                                                                                                                                                                                                                                                                                                                 63 LSNAAPIVLDIMRWGGIAYLLWF---AVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .20 SAVATD----TRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQ-Y 174
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                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                        1 MIAVYLHGFILSAAMILPLGPQNVPVWNQGIKRQHHLMSASLCALSDIILICAGIFGGSA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable transporter PA4365 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                    3 IMEIFITGLLLGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDL
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                                                                                        Query Match 28.1%; Score 335; DB 2; Length 205; Best Local Similarity 33.1%; Pred. No. 3.4e-23; Matches 80; Conservative 44; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.9%; Score 332; DB 2; Length 200; 33.5%; Pred. No. 6.2e-23;
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RESULT AG2690

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33;

QY 124 TDTRNRVEVEVSVDKQRVWVKPMLMAIVLTWILNPNAYLDAFVFIGGVGAQYGDTGRWIFA : : Db 109LW-QTLAICLALTFLNPHYXLDTVVLLGTISTQFPGFEK-TFA	
107	DTGRWIFA 183 A;Gene: Rv1986 C;Superfamily: Bscherichia coli hypothetical 23K protein (sbm-fba intergenic region)
184 AGAFAASLIWFPLVGFGAAALSRPLSSFKVWRWINVVVAVWMTALAIKIML 23	5A-1FA
Db 150 AGATGSLLFFFSLGYGARWLRPIFEKPSAWKILEGVIAITMWAIAFKLVM 200	2000 Qy 8 ITGLILGASLILSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTIGVDLISNAA 67
n Rv0488 - Mycobacterium tuberculogis (strain erium tuberculosis #sequence_revision 17-Jul-1998 #text_change	OY 68 PIVLDIMRMGGIAYILIMPAVAMAKOAMTNKVABAQIIEETEPTVPDDTPLGGSAVATDTR
C.Accession: C70744 R;Cole, S.T.; Ebrosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, I.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares,	C.; Harris, D.; Gordon, S.; Squares, D.; Harlin, N.; Holroyd, S. Db. 107LAEVLVICAAFTELINBHVXLDTVVLIGALANEHSDQ-RWLFGLGAV 151 S.; Squares, S.
Nature 343, 537-544, 1998 A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell A,Authors: Deciphering the biology of Mycobacterium tuberculosis from the A,Reference number: A70500; MUID:98295987; PMID:9634230	arrell, B.G. Qy 188 AASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVWHTALAIKI 232
not	not shown
Ajkesiumes: 1-201 (CDL) AjkToss-references: GB:277162; GB:AL123456; NID:g3261606; PIDN:CAB00949 AjkTosrimental source: strain H37Rv C;Genetics:	949.1; PID:g1449286
A;Gene: Rv0488 C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba interg	tergenic region)
Query Match 26.8%; Score 319; DB 2; Length 201; Best Local Similarity 32.4%; Pred. No. 9.6e-22; Matches 71; Conservative 50; Mismatches 64; Indels 34; Gap	Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A;Itle: The genome sequence of the facultative intracellular pathogen Brucell Gaps 4; A;Reference number: AD3252; PMID:11756688
QY 16 SILLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNAAPIVLDI 	A;ACCEBSION: AD3411 A;Ctatus: preliminary : : A;Molecule type: DNA PUNTLVAR 62 A;Residues: 1-204 <kur></kur>
OY 76 WGGIAYLLWFAVMAAKDAMTNKVBAPQIIEETEPTVPDDTPLGGSAVATDTRNRVRVE : : : : : : Db 63 FGGAAPTIGARANAWRPSGIVPSESGPAAL	VRVEVS 135
136 VDKQR	SLIWEP
Db 97IGVVQMCLVVTFLNPHVYLDTVVLIGALANEESDL-RWFFGAGAWAASVWFFA Ov 196 LVGFGAAALSRPLSSPKVWBWINVVAVWWTALAIXLML 234	148
:: :: : :: : :: : 149 VLGFSAGRLQPFFATPAAMRILDALVAVTMIGVAVVVLV	
RESULT 10 H70756 hypothetical protein Rv1986 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis	QY 68 PIVLDIMRWGGIAYLLWFAVMAAXDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATUTR
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: H70756 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hanlin, N.; Holroyd,	-Jun-2000
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squar, Nature 393, 537-544, 1998 A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell A; Title: Deciphering the biology of Mycobacterium tuberculosis from the brefarence number and the matth of Apple 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 1800 and 180	quares, S. rell, B.G. the complete genow
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serogroup O1	lers, F.J.;	H & B & H	C;Superfamily: Bscherichia coli hypothetical 23K protein (sbm-fba intergenic region) Query Match 14.8%; Score 176.5; DB 2; Length 220; Best Local Similarity 22.9%; Pred. No. 1e-08; Matches 53; Conservative 36; Mismatches 99; Indels 43; Gaps 4;	IFITGLLIGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIA	RESULT 15 F64609 conserved hypothetical integral membrane protein HP0718 - Helicobacter pylori (strain 26 C;Species: Halicobacter pylori C;Species: Halicobacter pylori C;Species: Halicobacter pylori C;Species: Halicobacter pylori C;Daces 109-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 17-Mar-2000 C;Accession: F64609 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Fleischmann, R.D. Nature 388, 539-547, 1997 A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Authors: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUD:97394467; PMID:9252185
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z, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, Kroph, S.; Hilbert, H.; Holasppel, S.; Galoson, S.; Hullo, M.F. Aroph, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, evic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetellt coeter, R.; Scofene, F.; Sekjauchi, J.; Sato, T.; Sato, T.; Sato, T.; Sekowska, A.; Sanon, Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, Yamane, M.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, I. Zumatenin, B.; Yoshikawa, H.; Danchin, A.; Tota, K.; Yoshida, I. Barquence of the Gram Posttive bacterium Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                       zer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterischi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc I.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
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68
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Pred. No. 1e-08;
5; Mismatches 99; Indels 43;
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3PK-----VWRW 216
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A,Molecule type: DNA
Kresiduse: 1-210 <TOM>
A;Cress-references: G-81,E000585; GB:AE000511; NID:92313845; PIDN:AAD07771.1; PID:9231384
C;Superfamily: Escherichia coli hypothetical 23K protein (8bm-fba intergenic region)
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                                                                                                                                                                                                                                             4 VFIEGFGLAISLCAAVGAQSLFIVERGMARNYVFLICALCFMCDIVLMSMGVFGVGAYF- 62
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                                                                                                              Query Match
14.6%; Score 173.5; DB 2; Length 210;
Best Local Similarity 21.9%; Pred. No. 1.8e-08;
Matches 51; Conservative 48; Mismatches 91; Indels 43; Gaps
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Search completed: March 12, 2004, 18:26:47 Job time : 21 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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33.5 33.6 33.6 33.7 33.8 33.9 33.9 40.5 41.0 80.5 44.0 80.5 44.0 80.5 44.0 80.5 44.0 80.5 44.0 80.5 44.0 80.5 80.5 80.5 80.5 80.5 80.5 80.5 80		LT 1 CORGL LYSE CORGL P94633; 15-JUL-1998 16-OCT-2001 28-FEB-2003 Lysine expox	Livis Ok CGALizez. Corynebacterium glv Bacteria; Actinobac Corynebacterineae; NCBI TaxID=1718;	SEQUENCE FROM N STRAID-R127, MEDLINE-9712681, VILLIC M.W., SAI "A new type of " lysine export fi Mol. Microbiol.	(Z) SEQUENCE FROI STRAIN≠ATCC : Nakagawa S ·	"Complete g "Complete g Submitted (-:- FUNCTIC NECESSA -:- SUBCELL	This SWISS-between the Buropea use by no modified an entities re or send an	EMBL; X9647 EMBL; X9647 EMBL; AP005 InterPro; I InterPro; I InterPro; I InterPro; I InterPro; I InterPro; I InterPro; I InterPro; I InterPro; I InterPro; I I InterPro; I I I I I I I I I I I I I I I I I I I
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64 SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVA 123
                                                                                                                                          4 MEIFITGLLIGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL 63
                                                                                                                                                                                                                                         124 TDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFA
                                                                                                                                                                                                                                                                                                 184 AGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                 24374 MW; 68FB379AB380EDA7 CRC64;
                                                                  Query Match 72.6%; Score 864.5; DB 1
Best Local Similarity 71.2%; Pred. No. 9.1e-68;
Matches 166; Conservative 30; Mismatches 32
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EMBL; AE000375; AAC75960.1; -.
EMBL; X14436; CAA32607.1; -.
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139 1
172 1
208 2
228 AA;
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                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
-!- SUBCELLUJAR LOCATION: Integral membrane protein. Inner membrane
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                                                                                                                                                                                                                 184 AGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
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-!- FINCTION: INVOLVED IN THE EFFLUX OF EXCESS OF L-LYSINE. TO NECESSARY TO CONTROL THE INTRACELLULAR L-LYSINE LEVEL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kimura E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723755; PubMed=12840036;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E Nishio Y., Atsui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori T.;
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
ILAQA H., Kimura E., Kawahara Y., Sugimoto S.;
"ILAGO, LyBE of Coryncheacerium efficiens.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
Pred. No. 7.1e-95; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (by brintaricy).
- - - SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                   228 AA
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EMBL; AP005218; BAC18167.1; ALT_INIT.
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                   233; Conservative
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STRAIN=K12 / CS220;
MEDLINE=89313302; PubMed=2546007;
Alefounder P.R., Baldwin S.A., Perham S.A., Short N.J.;
Alefounder P.R., Baldwin S.A., Perham S.A., Short N.J.;
Identification, molecular cloning and sequence analysis of a gene
cluster encoding the class II fructose 1,6-bisphosphate aldolase, 3-
phosphoglycerate kinase and a putative second glyceraldehyde 3-
phosphate dehydrogenase of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; Publed=9278503;
MEDLINE=97426617; Publed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOI. Microbiol. 3:723-732(1989).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
YGGA ECOLI STANDARD; PRT; 211 AA. P1657; D-0CT-1999 (Rel. 12, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
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SEQUENCE FROM N.A.
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MEDILINE-9825987; PubMede-9634230;
MEDILINE-9825987; PubMede-9634230;
MEDILINE-9825987; PubMede-9634230;
MEDILINE-9825987; PubMede-9634230;
MEDILINE-9825987; PubMede-9634230;
Gordon S. W., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Hornsby T., Devlin K., Fellwell T., McLean J., Moule S., Haurphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Sulston J.E., Taylor K., Whitehead S., Squares R.,
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gainn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                              75; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 AFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                 Length 211;
                                                                                                                                 Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                       2DAFE27B6A9BE822 CRC64;
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NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                    ch 29.4%; Score 350; DB 1;
1 Similarity 35.7%; Pred. No. 2.7e-23;
81; Conservative 37; Mismatches 75
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Hypothetical protein Rv0488/MT0507/Mb0498.
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01-0CT-1996 (Rel. 34, Last sequence update)
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              EcoGene; EG11159; yggA.
InterPro; IPR004777; Lys exporter.
InterPro: PP004123; LysE.
Pfan; PF01810; LysE; 1.
TIGREAMS; TIGR00948; 2a75; 1.
Hypothetical protein; Transmembrane;
                                                                                                                                                                                                                     111 131 POT
147 167 POT
179 199 POT
211 AA; 23175 MW; 2
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Nature 393:537-544(1998).
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88
B65077; QQEC5A.
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MEDLINE=22709107; PubMed=1218/897;
MEDLINE=22709107; PubMed=1218/8979.

MEDLINE=2209107; PubMed=1218/8979.

Paroi M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Paroi M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Parkill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis.";

"The complete genome sequence of Mycobacterium bovis.";

Proc. NAIL, Acad. Sci. U.S.A. 100:7877-7882(2003).

-: SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-: SIMILARITY: BELOWS 70 THE LYSE/NGGA PAMILY.
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
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01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein Rv1986/MT2040/MD2048.
RV1986 OR MT2040 OR MTCY39.33C OR MB2008.
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InterPro; IPR004777; Lys exporter.
InterPro; IPR001123; LysE.
                                                                                                J. Bacteriol. 184:5479-5490(2002)
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EMBL; AE006952; AAK44730.1; -.
EMBL; BX248335; CAD93361.1; -.
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TIGRFAMs; TIGR00948; 2a75; 1.
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153
189
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Best Local Similarity
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                                                                                                                 MEDILINE=88295987; PubMed=9634230;
Garnier T., Churcher C., Harris D.,
Gordon S.V., Eroseh R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Enown D., Chillingworth T., Connor R.,
Badcock K., Besham D., Erown D., Chillingworth T., Connor R.,
Brown D., Chillingworth T., Connor R.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Hurphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Bulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES-M. Dovis; STRAIN-AF2122/97;
MEDLINE-22709107; PubMed=12788972;
Garnier T., Elgimeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Arkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genrome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7897-7882 (2003).
-: SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                 SPECIES-M. tuberculosis, STRAIN-CDC 1551 / Oshkosh,
MEDLINE-22206494; PubMed-12218036,
Relsichmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraeer C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                           Bacteria: Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI TaxID=1773, 1765;
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                                                                                                       SPECIES=M.tuberculosia; STRAIN=H37Rv;
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InterPro; IPR004777; Lys exporter.
InterPro; IPR001123; LysE.
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    Mycobacterium tuberculosis, and
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TIGRFAMS; TIGR00948; 2a75; 1.
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                   Mycobacterium bovis.
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199 AA;
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                                                                                                                                                                                                                                                        128 NRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAAGAF 187
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                                                                                                                  6 vvGrLACFTLIAAIGAQNAFVLRQGIQREHVLPVVALCTVSDIVLIAAGIAGFGALIGAH 65
                                                                     8 ITGLILICASLILISIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNAA
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                        34; Gaps
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MEDLINE-97431471; PubMed-9286976;
Swift S., Karlyahev A.V., Fish L., Durant E.L., Winson M.K.,
Chhabra S.R., Williams P., Macintyre S., Stewart G.S.A.B.;
"Quorum sensing in Aeromonas hydrophila and Aeromonas salmonicida:
identification of the LuxRI homologs AhyRI and AsaRI and their
cognate N-acylhomoserine lactone signal molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 179:5271-5281(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
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Aeromonadaceae; Aeromonas.
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                                                                                                                                                                                                                                                                                                                                                       188 AASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL 232
                                                                                                                                                                                                                                                                                                                                                                               31.1%; Pred. No. 1.5e-20; ive 44; Mismatches 77; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                 66 PRALINVVKFGGAAFLIGYGLLAARRAWRPVALIP-
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InterPro; IPR004777; Lys exporter.
InterPro; IPR001123; LysE.
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                             70; Conservative
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TIGRFAMs; TIGR00948;
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206 AA;
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15-JUL-1998
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8 ITGLILGASILLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNAA 67

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Length 199;

26.7%; Score 318; DB 1;

Query Match

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124 TDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFA 183
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WIRDILNE-115623! PubMed=11528196;
Hayashi T., Patkino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Saeakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIJINE-92358234, PubMed=1379743;
MEDIJINE-92358234, PubMedt G. III, Burland V.D., Blattner F.R.;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region
from 84.5 to 86.5 minutes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Harkett J., Klink S., Boutin A., Shao Y., Miller L., Agrocheck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterobaemorrhagic Escherichia coli 0157:H7.";
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Bacherichia coli, and
Bacherichia coli 0157:147.
Bacteria: Proteobacteria: Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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STRALT12,
MEDLINE-8711514; PubMed=3027506;
Irino N., Nakayama K., Nakayama H.;
"The rec' gene of Escherichia coli K12: primary structure and evidence for SOS regulation.";
MOI. Gen. Genet. 205:298-304(1986).
                                                                                                                          150 AVAMLASLVWFYSLAFGAVVLSPWLARSRQGYSKLIILLLVSPCWGW 196
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Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                    (Rel. 23, Created)
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                         184 AGAFAASLIWFPLVGFGAAALSRPLSSPK-----
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STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; Pubmed=11206551;
                                                                                                                                                                                                                    PRT;
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RHTC OR B3823 OR Z5344 OR ECS4753.
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                                                                                                                                                                                                                    STANDARD;
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STRAIN=K12 / MG1655;
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15-JUL-1998 (
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REVISIONS.
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                                                       PIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDTR 127
                                                                                         ----GAALADSPR 104
                                                                                                                            128 NRVRVEVSVDKQRVWVKPML-MAIVLTWINPNAYLDAFVFIGGVGAQYGDTGRWIFAAGA 186
                                                                                                                                                              105 ------LMGVKSVLAMTLGVTLLNPHVYLDTLMLLGSFGSQFAEPLRPAFAGA 152
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6 LQGFTLGLAMIIPIGAQNAFVLSRGIHRNHHLAATLCCLCDLILIGIGVFGGANLLAAS 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDITRE 97431471; PubMed=9286976; Swift S., Karlyshev A.V., Fish L., Durant E.L., Winson M.K., Chhabra S.R., Williams P., Macinityre S., Stewart G.S.J.B.; Chhabra S.R., Williams P., Macinityre S., Stewart G.S.J.B.; Guorum sensing in Aeromonas hydrophila and Aeromonas salmonicida: identification of the LuxRI homologs AhyRI and AsaRI and their cognate N-acylhomoserine lactone signal molecules."; J. Bacteriol. 179:5271-5281(1997).
-: SUBCELLULAR LOCATION: Integral membrane protein (Probable).
                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Hypothetical 24.5 kDa protein in ahyR-cdpD intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
Aeromonadaceae; Aeromonas.
                                                                                                                                                                                                187 FAASLIWFPLVGFGAALSRPLSSPKVWRWINVVVAVVMTALAIKL 232
                                                                                                                                                                                                                       153 MLASLVWFYSLAFGAAALSPWLARGRVOOAIDTIVGLIMLGLALOL 198
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Pred. No. 5.8e-15;
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InterPro; IPR001123; LysE.
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TIGREAMS; TIGR00948; 2a75; 1.
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125 AA;
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Best Local Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 VATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNA---YLDAFVFIGGVGAQYGDTG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 LLGASLLLSI-GPONVLVIKQGIK---REGLIAVLLVCLISDVFLFIAGTLGVDLLSNAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 LVGAIFIVLVPGPNTLFVLKNSVSSGMKGGYLAACGVFIGDAVLMFLAWA-GVATLIKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 PIVLDIMRWGGIAYLLW-----FAVMAAKDAMTNKVEAPQIIBETEPTVPDDTPLGGSA
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97251358; PubMed=9097040;
MEDLINE-97251358; PubMed=9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Rimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Salto N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Mada C., Yamamoto Y., Horiuchi T.;
'A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Greegor M., Daris N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Bscherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 3:379-392(1996).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the rht family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.5%; Score 101; DB 1; Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342E0DF348C9AD9A CRC64;
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40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, D90823, BAA15593.1; -.
EMBL, D90824; BAA15602.1; -.
PIR, F64940; F64940.
ECGGene, EG13505; yeas.
InterPro; IPR001123, LysE.
Pfam, PF01810; LysE; 1.
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                     Hypothetical protein yeas
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91
142
173
208
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188 2
212 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                               Sscherichia coli.
                                                                                                                                    NCBI_TaxID=562;
                                            (EAS OR B1798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
                                                                                                                                                                                                         STRAIN=K12
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                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 VDLLSNAAPIVLDIMRW-----GGIAYLLWFAVMAAKDAMINK---VEAPQIIEETEP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHL-----11EKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQV----- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 -----ELAKSGRS-----FINGLLTNLANPK----AIIYFGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 VFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGAL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 TVPDDTPLGGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 -----VGAQYGDTGRWIFPAGAFASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 IMEIFITGLLLGASLLLSIGPQNVLVIKQGIKR---EGLIAVLLVCLISDVFLFIAGTLG 59
                                                                                                                                                            FEBS Lett. 452:228-232(1999).

-!- FUNCTION: CONDUCTS THE EFFLUX OF THREONINE.

-!- SUGCELLULAR LOCATION: Integral membrane protein (Potential).

-!- SIMILARITY: Belongs to the rht family.

-!- CAUTION: Ref. 2 sequence differs from that shown due to a frameshift in position 80.

-!- CAUTION: Ref. 9 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS IN POSITIONS 47 AND 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MIMIFLIVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIA-LLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64; Gaps
                                                                                                               The novel transmembrane Escherichia coli proteins involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 8.8%; Score 105; DB 1; Length 206; 1 Similarity 20.4%; Pred. No. 0.041; 51; Conservative 36; Mismatches 99; Indels 6
                                                             Zakataeva N.P., Aleshin V.V., Tokmakova I.L., Troshin P.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22474 MW; F64017878CC6D50D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEAS_ECOLI STANDARD; PRT; 212 AA P76249; 007969; 007971, Created)
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport; Transmembrane; Complete proteome.
TRANSMEM 1 21 POTENTIAL.
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EMBL; AE000458; AAC76826.1; ALT_FRAME.
EMBL; AE005613; AAG59019.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP002567; BAB38176.1; -.
EMBL; M30198; -; NOT_ANNOTATED_CDS.
PIR; A98223; A98223.
Excogene; EG11468; rhtC.
InterPro; IPR004778; Homoser_Thr_eff.
InterPro; IPR001123; LysE.
                                                    MEDLINE=99313167; PubMed=10386596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01810; LysB; 1.
TIGRFAMS; TIGR00949; 2A76; 1.
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                                                                                                                                             amino acid efflux.";
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MEDLINE=91227627; Pubmed=2092358;
Relzer J., Reizer A., Saier W.H. Jr.;
Relzer J. and tespes permease of Encherichia coli consists of three proteins and is homologous to the lactose permease of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keyhani N.O., Wang L.-X., Lee Y.C., Roseman S.,
"The chitin disaccharide, N,N'-diacetylchitobiose, is catabolized by
Bscherichia coli and is transported/phosphorylated by the
phosphoenolpyruvate:glycose phosphotransferase system.";
                                                                                                                                              PICC ECOLI STANDARD;
P17354; p762072: p76907; p71332;
01.AUG-1990 (Rel. 15, Created)
10.NCV-1997 (Rel. 15, Last sequence update)
10.OCT-2003 (Rel. 42, Last annotation update)
PTS system, N.N. -diacetylchitobiose-specific IIC component (BIIC-Chb)
(N.N. -diacetylchitobiose-permease IIC component (Phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parker L.L., Hall B.G., "Characterization and nucleotide sequence of the cryptic cel operon of Escherichia coli K12."; of Escherichia coli K12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-KLZ / MGG555,
MEDLINE-SY426617; DAG6557,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor M., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
179 RWIFAA----SLIWFPLVGFGA 201
                                   153 FFILAATLELVSFCYLSFLIISGAFVTQYIRTKKKLAKVGNSLIGLMFVGFAA 205
                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keyhani N.O., Roseman S.;
Wild-Cype Bacherichia coli grows on the chitin disaccharide,
"Wild-diacetylchitobioes, by expressing the cel operon.";
Proc. Natl. Acad. Sci. U.S.A. 94:14367-14371(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Res. Microbiol. 141:1061-1067(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20490752; PubMed=10913117;
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MEDLINE=98070757; PubMed=9405618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90185127; PubMed=2179047;
                                                                                                                                                                                                                                                                                                                                                                                     Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequen
Science 277:1453-1474(1997)
                                                                                                                                                                                                                                                                                                  enzyme II, C component).
CHBC OR CELB OR B1737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 WGTNFHOIIMDTISTPLASLGSVVGWAYVIFVPLLWFFGIHGALALTALDNGIMTPWALE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 ITGLILG---ASLILSIGPONVLV----IKQGIKR--EGLIAVLLVCLISDVFLFIAGT 57
J. Biol. Chem. 275:33084-33090 (2000).

-!- FUNCTION: This is a component of the phosphoenolpyruvate-dependent sugar phosphotransferase system (FTS), a major carbohydrate active-transport system. The IICD domains contain the sugar binding site and the transmembrane channel; the IIA domain contains the primary phosphorylation site (the donor is phospho-HPr); IIA transfers its phosphoryl group to the IIB domain which finally transfers it to
                                                                                                                                                                                                    -!- PATHWAY: N,N'-diacetylchitobiose utilization.
-!- SIMECELULAR LOCATION: Integral membrane protein. Inner membrane.
-!- INDUCTION: By N,N'-diacetylchitobiose.
-!- SIMILARITY: Contains 1 FTS ELIC domain.
-!- CAUTION: Was originally (Ref. 4) characterized as part of a cryptic cel operon for a cellobiose degradation system. The Cel+ phenotype is due to mutations making expression chitobiose-independent and altering the substrate specificity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVAALLVALFNLGIATLIYLPFVVVANKAQNAIDKEESEED
IANALKF -> TSPHCWSHSSTLASQR (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> LSTALVLRIHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIPGFIILSVMGIIAW -> FNSRLYYSFRDGDYCL (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93.5; DB 1; Length 452; Pred. No. 0.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfan; PF02378; PTS_EIIC; 1.
TIGRFAMs; TIGR00359; Cello_pts_IIC; 1.
TIGRFAMs; TIGR00410; lacs; 1.
Phosphotransferase system; Sugar transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVLVQP -> LYWYNR (IN REF. 1)
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FVPLLWFFGHGALALTALDNGIMTP
ACADRTGQRHYDA (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 452 AA; 48332 MW; EC3CBFEED6231068 CRC64;
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InterPro; IPR004796; Cello_pts_IIC.
InterPro; IPR004352; Ptrans_EIIC.
InterPro; IPR00451; Pts_lac.
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EMBL; D90816, BAA15518.1; -.
EMBL; D90817, BAA15526.1; -.
EMBL; D90818; BAA15532.1; -.
PIR; A64933; A64933.
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hes 52; Conservative
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ELG, H64755, H64759.
ECGGene; EG13598; yah.
IncerPro; IPR004778; Homoser_Thr_eff.
                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae; Escherichia.
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TIGRFAMS; TIGR00949; 2A76; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001123; LysE.
                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein yahN
                                                        47; Conservative
                                                                                                                                                                                                                                                                                                     STANDARD;
                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                       YAHN ECOLI
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 TRANSMEM
SEQUENCE
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                                   Query Match
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                                                         Matches
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 106 ETEPTVPDDTPLGGSAVAT-DTRNRVRVEVSVDKQ-RVWVKPMLMAIVLTWLNPNAYLDA 163
                        -----IDS 300
                                             ---AQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPL 208
                                                            Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Goditer T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Theboult P., Vandenbol M., Weidner S., Galibert F.; Manlysis G. the chronosome sequence of the legume symbiont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERMEASE 1; FALSE NEG.
51t; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                         Powers E.L., Vuyyuru V., Kahn M.L.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                        ----IATYQQYGSVEAALAAGKTFHIWAKPM
                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical transport protein R00093.
R00093 OR SMC02616.
Rhizobium meliloti (Sinorhizobium meliloti)
                                                                                                                                                                           465 AA.
                                                                                                                 357 MFIPF----VLVQPILAAITLAAYYMG 379
                                                                                             209 SSPKVWRWINVVVAVVMTALAIKLMLMG 236
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InterPro; IRR004840; AAC_permease.
InterPro; IRR004841; Permease region.
Pfam; PF00324; aa_permeases; I
PROSITE; PS00218; AMINO ALID PERMEASE I
Hypothetical protein; Transport; Trans
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                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70
1111
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383
                                               164 FVFIGGVG-----
                         270 N-----
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164
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244
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                                                                                                                                                                                                                                                                                                                                STRAIN=1021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 DDTPLGGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 -----VGFLLDTVAGMQGQTGLNQOPFIV---LAIMPLAMLNYRGVLATLTF---- 162
                                                                                                                                                                                                                                                                                                                                                                                                                   64 SNAAP-----IVLDIMRWG-GIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVP 112
                                                                                                                                                                                                                                                          17 LLLSIGPQNVLVIKQGI------KREGLIAVLLVCLISDVFLFIAGTLGVDLL 63
                                                                                                                                                                                                                                                                                                                                      16 LLRVIGPAHVWALGVGIVLVGEYMGWNFSVGKGCMIAGLMACWVAGLLYTCVAMIDSEVT
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 QYGDIGRWIFAAGAFAASLIWFPLVGFGAAAL----SRPLSSPKVWRWINVVAV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Killey M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oefner P., Roberte D., Schrama S., Davis R.W.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-: SIMILARITY: Belongs to the rht family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                             67;
                                                                                                        Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Transmembrane; Complete proteome.
403 423 POTENTIAL.
465 AA; 50783 MW; 0375E164F737AA0A CRC64;
                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P75693; P71307; Ol. NOV-1997 (Rel. 35, Created) 01.NOV-1997 (Rel. 35, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                    7.8%; Score 92.5; DB 20.0%; Pred. No. 1.1; tive 38; Mismatches
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21
64 POY
87 POY
173 POY
22498 MW;
                                                                            7.68;
                                                                                                     Conservative
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    1
44
67
150
206 AA;
                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                     229 AIKLML 234
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                                                                                                                 10;
                                                                                                                                                                                          66 AAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEP-TVPDDTPLGGSAVAT 124
                                                                                                                                                                                                                                           125 DTRNRVRVEVSYDKORVWVKPMLMAIVLTWLNPNAYLDAFVFIGGV--GAQYGDTGRWIF 182
                                                                                                                                                                                                                                                                     -----WYVFFRRGLITDLSNPQTVL-FFISIFSVTLNAETPTWARLMA 165
                                                                                                                                         11 LLLGASLLLSIGP-QNVLVIKQ----GIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSN 65
                                                                                                                                                       | :| :: | |: |: |: |
LIVGLFVITFFNPGANLFVVVQTSLASGRRAGVLIGLGVAL-GDAFYSGLGLFGLATLIT 80
                                                                                                                 48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=21534946; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                              166 WAGIVLASIIWRVFLSQAFSLPAVRRAYG--RWQRVASRVIGAIIGVFALRLIYEG 219
                                                                                                                                                                                                                                                                                             183 AAGAFAASLIW--FPLVGFGAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: CONDUCTS THE EFFLUX OF THREONINE (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the rht family.
                                                                                                                                                                                                                  81 QCEEIFSLIRIVGGÄYLLWFAWCSMRRQST-----PQMSTLQQPISAP----
            POTENTIAL.
POTENTIAL.
POTENTIAL.
LELIYEGYTOR -> YA (IN REF. 2).
B17F5ABC31E83F26 CRC64;
                                                                                       ; Score 92; DB 1; Length 223;
; Pred. No. 0.59;
33; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transport; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                     206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro, IPR004778; Homoser_Thr_eff.
InterPro, IPR001123; LyeB.
Pfam; PF01810; LyeB; 1,
TIGRPAMS; TIGR00949; 2A76; 1.
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF233324; AAF33433.1; -.
                                                             24811 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE008884; AAL22803.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
                                                                                    7.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Threonine efflux protein. RHTC OR STM3959 OR STMD1.31.
                                                                                                   22.9%;
                                                                                                                54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:852-856(2001)
42
105
184
223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhimurium.
                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                     SALTY
                                  TRANSMEM
CONFLICT
SEQUENCE
                                                                                                                                                                22
TRANSMEM
TRANSMEM
                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                     RHTC SI
09L6N7
                                                                                                                Matches
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 SHHHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNK---VEAPQIIBETEPTVPDDTPL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 GGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGG-----VGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 ---ELAQSGRS------FLKGLLTNLSNPK----AIIYFGSVFSLFVGD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 QYGDTGRWIFAAGAFA----ASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTAL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 NVGAAARW----GIFALITLETLAWFTVVASLFALPKWRRGYQRLAKWIDGFAGALFAGF 198
                                                                                                                                                                                                                                                                                                                               09
                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                    3 IMELFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGT--LGV
                                                                                                                                                                                                                                                                                                                                                                     { (1,4) - (N-acetyl-
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LÓCATION: Integral membrane protein. Plasma membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Din A.B., Yarden O.; "The Neurospora crassa chs-2 gene encodes a non-essential chitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
Chitin synthase 2 (BC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl transferase 2)
                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurospora crassa.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 89:519-523 (1992).
-!- FUNCTION: Plays a major role in cell wall biogenesis.
-!- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + { (1,4) - (N glucosaminyl) } (N) = UDP + { (1,4) - (N glucosaminyl) } (N+1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bowen A.R., Chen-Wu J.L., Momany M., Young R., Szaniszlo P.J.,
Robbins P.W.;
                                                                                                                                                                                Score 91; DB 1; Length 206;
                                                                                                                                                                                                           20.3%; Pred. No. u.bo;
tive 34; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 HLIIEKWAWLHTIIMVGGGLYLCWMGYQMLRGALKKQDAAASSPHI
                                                                   POTENTIAL.
080477853FC2733F CRC64;

    -!- SIMILARITY: Belongs to the chitin synthase family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Classification of fungal chitin synthages.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          944 AA.
POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92115692; PubMed=1731323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbiology 140:2189-2197(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 250-438 FROM N.A.
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MEDLINE=90062147; PubMed=2584214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal; Alternative splicing. signat.
                                                                                                                                                                                                                                                                        EMBL; M24282; AAA03201.1; -. PIR; A37797; A37797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3137
2042
2379
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1014
1207
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1621
1814
2029
2587
2821
3043
3137
2172
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                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00014; Kunitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
444
644
644
1035
11239
11239
11441
11641
11641
2407
22625
22945
2166
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26
2043
2380
38
                                                                                                                  Name=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
 126
                                                                                                                                                                                                                            641 YVCVLLICTQFILSLGNR-----PQGAKRMYLASMIIYAVİMVYTTFATIFIVVRQIQPS 695
                                                                                                                                                                                                                                               -----TLGVDLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMINKVE----APQI 103
                                                                                                                                                                                                                                                                                                                           127 -RNRVRV---EVSVDK-QRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWI 181
                                                                                                                                                                                                          7 FITGLLIGASLLLSIGPONVLVIKOGIKREGLIAVLLVCLI-----SDVFLFIAG---- 56
                                                                                                                                                                                                                                                           753 ICTLOIYAFCNTHDVTWGTKGDNVMRTDLGGAIVKGSTVELEMPSDQLDIDSGYDECLRN
                                                                                                                                                                                                                                                                                                                                             813 LRDRVMVPCRSLSEDOLQQDYYKSVRTYMVVSWMVANATLAM-----AVSEAYGDSE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                       54; Mismatches 95; Indels 86; Gaps
                                                                                                                                                                                                                                                                                                                                                                    182 FAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMIMG 236
                                                                                                                                                                                                                                                                                                                                                                             865 IGDNFYLRFILM----AVAALALFRALGS-TTFAAINLVSALVEGRVRLRLNMKG 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90212613; PubMed-2322559;
Bonaldo P., Russo V., Bucciotti F., Doliana R., Colombatti A.;
"Structural and functional features of the alpha 3 chain indicate a
bridging role for chicken collagen VI in connective tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doliana R., Bonaido P., Colombatti A., "Multiple forms of chicken alpha 3(VI) collagen chain generated by alternative splicing in type A repeated domains.";

Cell Biol. 111:2197-2205 (1990).
                                                InterPro; IPR004834; Chitin_synth.
Pfam; PF01644; Chitin_synth; 1.
ProDom; PD002998; Chitin_synth; 1.
Transferase; Glycosyltransferase; Transmembrane; Cell wall;
                                                                                                                                                                   Score 89; DB 1; Length 944;
Pred. No. 4.7;
                                                                                                                                                 106816 MW; F70052AEE083060D CRC64;
                                                                                                                                                                                                                                                                                       ---EETEPTVPDD---TPLGGSAVATDT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR 1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 3137 AA.
                                                                                                 POTENTIAL
                                                                                                           POTENTIAL
                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collagen alpha 3(VI) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91035630; PubMed=1977751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 29:1245-1254(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [3]
SEQUENCE OF 2871-3137 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 224-2871 FROM N.A.
          EMBL; X77782; CAA54816.1; -.
EMBL; M82951; AAA3382.1; -.
PIR; B45189; B45189.
PIR; T47246; T47246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] -
SEQUENCE OF 1-853 FROM N.A.
                                                                                                                                                                             Local Similarity 20.3 tes 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
                                                                                                 617
654
689
733
893
                                                                                                                                                 944 AA;
                                                                                                                                                                                                                                                                                       104 I-----
                                                                                       Multigene family.
TRANSMEM 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                    699
                                                                                                                                                                                                                                                                                                                                                                                                                                      CA36 CHICK
P15989;
                                                                                                                                                                                                                                                 57
                                                                                                                                                SEQUENCE
                                                                                                                                                                     Query Match
                                                                                                           TRANSMEM
                                                                                                                    TRANSMEM
                                                                                                                               TRANSMEM
                                                                                                                                        TRANSMEM
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                                                                                                                                                                                       Matches
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Bonaldo P., Colombatti A.;
"The carboxyl terminus of the chicken alpha 3 chain of collagen VI is "The carboxyl terminus of the chicken alpha 3 chain of collagen VI is aunique mosaic structure with glycoprotein Ib-like, fibronectin type III, and Kunitz modules.";
J. Biol. Chem. 264:20235-20239(1989).
-!- FUNCTION: Collagen VI acts as a cell-binding protein.
-!- SUBUNIT: Trimers composed of three different chains: alpha 1(VI), and alpha alpha 3(VI).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains - :- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain. -:- SIMILARITY: Contains 1 Elbronectin type III domain. -:- SIMILARITY: Contains 1 Elbronectin type III domain. -:- SIMILARITY: Contains 12 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Cell adhesion; Serine protease inhibitor; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIBRONECTIN TYPE-III.
BPTI/KUNITZ INHIBITOR.
INTERRUPTION IN COLLAGENOUS REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLLAGEN ALPHA 3 (VI) CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NONHELICAL REGION.
TRIPLE-HELICAL REGION.
NONHELICAL REGION.
                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=1;
Comment=At least 2 isoforms are produced;
                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P15989-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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VWFA 2.
VWFA 3.
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VWFA 5.
VWFA 6.
VWFA 7.
VWFA 8.
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SWART; SM00131; KU; 1.

SWART; SM00321; VWA; 12.

PROSITE; PS00280; BFTI KUNITZ 1; 1.

PROSITE; PS50279; BPTI KUNITZ 2; 1.

PROSITE; PS50234; VWFA; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, P12111, ZKMT.
InterPro; IPR003161; Clg helix.
InterPro; IPR003161; Collagen.
InterPro; IPR003961; FN III.
InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR002235; WWP_A.
Pfam; PP01301; Collagen; 6.
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PRINTS; PR00759; BASICPTASE.
PRINTS; PR00453; VWFADOMAIN.
ProDom; PD0000007; Clg helix; 1.
ProDom; PD000222; Kunitz_BFII; 1.
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                            119 GSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTG 178
                                                                                                                                                                                                                                                                                                                                                                                                         393 TDGSFAFTALDIRNLAALRELLLPNIVGVAQRLI-LLEAPTIVTEVIEVNKKDIVFLIDG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------ÀQYADTV 492
                                                                                                                                                                                                                                                                                                                           14 GASLLLSIGPONVLVIKOGIK----REGLIAVLLVCLISDVFLFIAGTLGVDLL----- 63
                                                                                                                                                                                                                                                                 Query Match 7.4%; Score 88.5; DB 1; Length 3137; Best Local Similarity 25.4%; Pred. No. 18; Matches 46; Conservative 22; Mismatches 74; Indels 39; Gaps
INTERRUPTION IN COLLAGENOUS REGION.
INTERRUPTION IN COLLAGENOUS REGION.
CELL ATTACHNENT SITE.
CELL ATTACHNENT SITE.
CELL ATTACHMENT SITE.
REACTIVE BOND (BY SIMILARITY).
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Search completed: March 12, 2004, 18:25:16 Job time: 19 secs

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A. Weissenbach J., Boucher C.A.;
I. "Genome sequence of the plant pathogen Ralstonia solanacearum.";
I. Nature 415.497-502(2002).
R. EMBL; ALG46067; CAD15726.1;
C. EMBL; ALG46067; Camenbrane; IEA.
R. GO: GO:0016029; F:lyaine permease activity; IEA.
R. GO: GO:0006855; P:pamino acid transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                       Raistonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Ralstonia.
               Q8g1n8
Q9ckj7
Q87115
Q8dc97
Q7wg70
Q7wg40
Q7wg40
Q7wg40
Q9kun4
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Q9zlc4
Q99vil
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097fy1
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Q8nxi2
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Q88hc2
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                           202 AA.
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         08ED97
08GIN8
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07VS78
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07WIN4
09GT30
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08RKZ2
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Q8EG90
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MEDLINE=21681879; Pubmed=11823852;
                                                                                                                                                                                                                                                                                                                                                      Probable transmembrane protein. RSC2024 OR RS03592.
InterPro; IPR001123; LybE. Pfam; PF01810; LybE; 1. Complete proteome.
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Best Local Similarity
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NCBI TaxID=305;
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Qrubge Maigella fi
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Qahw36 peseudomonas
Qay4k6 streptomyce
Qspws xanthomonas
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Q8fe55 escherichia
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Q88pd4
Q8p613
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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NCBI TaxID=601;
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                                    VLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDTRNR 129
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65 SPWILLALVTWGGVAFLLWYGFGAFKTAMSSNIÈL-------
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MEDLINE=22388234; PubMed=12471157;
Welch R., Burland V., Plunkett C. III, Redford P., Roesch P.,
Welch R., Burland V., Dlunkett C., Boutin A., Hackett J., Stroud D.,
Mayhew G.R., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.I.T., Donnenberg M.S., Blattner F.R.;
"Extensive measuic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 29.1%; Score 347; DB 16; Length 211;
l Similarity 35.7%; Pred. No. 2.6e-22;
B1; Conservative 37; Mismatches 75; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                  ASLIWFPLVGFGAALSRPL-SSPKVWRWINVVVAVVMTALAIKLMLM 235
                                                                                                                                                 .86 AFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL
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Last sequence update)
Last annotation update)
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GO; GO:0016293; F:lysine permease activity; IEA.
GO; GO:0006565; P:amino acid transport; IEA.
InterPro; IPR003016; Lipoyl BS.
InterPro; IPR001123; LySE.
                                                                                                                                                                                                                      211 AA
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SEQUENCE 211 AA; 23173 MW; 5F22D06A3
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                                                    ::|: |:|| |::||: :
67 IVDVARYGGAAFILWYGI----
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TIGRFAMS; TIGR00948; 2a75; 1.
PROSITE; PS00189; LIPOYL; 1.
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SEQUENCE FROM N.A.
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63 LSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAV 122
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STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMed=12644504;
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2"
                                                                                                                                                                                                                                                                                                                                                                                                                      Wain J.,
                                                                                                                                                                                                                                                                                                                                                                                                        Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Bashama D., Baroks K., Chillingworth T., Comnerton P., Cronin A., Davies R.M., Dowd L., White N., Farrar J., Peltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., Whitehead S., Barrell B.G., Each M., Skelton J., Stevens K., Whitehead S., Barrell B.G., Multiple drug resistant Salmonella enterica serovar Typhi CT18.";
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                                                                          Last sequence update)
Last annotation update)
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Pred. No. 2.6e-22;
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EMBL, AL627277; CAD02896.1; -.

EMBL, AE016844; AA070556.1; -.

GO, GO:001601; C:integral to membrane; IEA.

GO; GO:00106293; F:lysine permease activity; IEA.

GO: GO:0006865; P:amino acid transport; IEA.
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211 AA.
                                                     Created)
                                                                                                                                     Possible membrane transport protein.
STY3222 OR T2984.
Salmonella typhi.
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TIGRFAMS; TIGR00948; 2a75; 1.
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33.6%;
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                                                                                                       01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR004777;
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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99 ------ASAEVMKQGRW-KIIATMLAVTWLNPHVYLDTFVVLGSLGGQLAMEPKRW- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 LSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 AIDIRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYG-DIGRWI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 IMELFITGLLLGASLLLSIGPQNVLVIKQCIKREGLIAVLLVCLISDVFLFIAGTLGVDL 62
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MEDLINE-21156231; PubMed-11258736;
MEDLINE-21156231; PubMed-11258736;
MEDLINE-21156231; PubMed-11258736;
Hand C. G., Ohribbo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sabakawa C., Oqusawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
EMBL; AE005522; AAGS8049.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 FAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perra N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Roge D.J., Maylew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hazkett J., Klink S., Boutin A., Shao V., Miller L., Agrocheck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                       Length 211;
                                                                                              EMBL; AE008841; AAL21941.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0006865; P:lysine permease activity; IEA.

GO; GO:0006865; P:auino acid transport; IEA.

InterPro; IPR004773; Lys.

InterPro; IPR004773; Lys.

Ffam; PF01810; LysE; 1.

ITGREMM; TISR00494; 2375; 1.

Hypothetical protein; Complete protecome.

SEQUENCE. 211 AA, 23220 MW; 64D6FC8FF21FIDDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LIMOSPWILLALVTWGGVAFILWYGFGALKTAMSSNLEL------
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                       29.1%; Score 346; DB 16; 33.6%; Pred. No. 3.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orf, hypothetical protein. YGGA OR Z4260 OR ECS3794. Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 33.69
Les 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                           Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=0157:H7 / El
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 NPTLLAVARWGGVIFLTHYGLQALRRACSR-----QSLEH-------SAAAGT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAAGA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 FITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 YFNGLLIAAGLIMAIGTQNAFVLAQGLRREHHVPVAMLCVVCDAILVAAGVFGLANVLAH 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21534948; PubMed-11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courney L., Porvollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal M., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.1%; Score 346; DB 16; Length 200;
33.0%; Pred. No. 2.9e-22;
tive 48; Mismatches 70; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                 Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M., Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S., White O., Enasan M., Haft D., Selengut J., Nelson W., Davidsen T., White O., Fraser C., Collmer A.; Selengut J., Nelson W., Davidsen T., Submitted (WAR-2003) to the EMBL, Genbank/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                  tomato).
Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 FAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 AA; 21339 MW; BB24A1AE402C0880 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-UNV-2003 (TrEMBLrel. 24, Last annotation update) Putative LYSE family, amino acid transport protein. YGGA OR STW3066.
                                             (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016020; C:membrane; IEA.
GO; GO:0005293; F:lysine permease activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
  200 AA.
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01-MAR-2002 (TrEMBLrel. 20, Last seq
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  PRT;
                                                                                                                                                                                                                                  Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001123; LysE. Pfam; PF01810; LysE; 1.
                                                                                                                                                                                  Pseudomonas syringae (pv.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 33.0%
Matches 75; Conservative
                                                                                                                              Transporter, LysE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                             NCBI_TaxID=323;
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                                                                                                                                                                                                                                                                                                                                         STRAIN=DC3000;
                                                     01-JUN-2003
                                                                                                   01-OCT-2003
                                                                                                                                                         PSPT04362
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68 PIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDTR 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 RNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYG-DTGRWIFAAG 185
                                                                                                            99 -----ASAEVLKÓGRW-KIIATMLAVTWLNPHVÝLDTRVVLGSLGGOLDVEPKRW-FALG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X MEDLINE-21681879; PubMed=11823852; X MEDLINE-21681879; PubMed=11823852; Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Salanoubat M., Genin S., Artiguenave F., Camus J.C., Cattolico L., Arlat M., Ebilault A., Brottier P., Camus J.C., Cunnac S., Demarge N., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demarge N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Signier P., Thebault P., Whalen M., Wincker P., Levy M., Reissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Mature 415.497-502(2002).

R EMBL, AL646059; CAD13913.1; -. Gol Go.0016020; Cmembrane; IEA.

RO; Go.0005293; F.!ysine permease activity; IEA.

RO; GO:0005283; F.!ysine permease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 ITGLLLGASLLLSIGPONVLVIKOGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, RalBtonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.2%; Score 336; DB 16; Length 212; 31.0%; Pred. No. 2.3e-21; tive 44; Mismatches 82; Indels 35
                                                                                                                                                                                    186 AFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 212 AA; 21896 MW; E29D663C9497EDBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-VAN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2019 (TrEMBLrel. 24, Last annotation update)
RSC0385 OR RS03353.
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(TrEMBLrel. 20, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ralstonia solanacearum (Pseudomonas solanacearum)
205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 PAWLTAVRWAGAAFLLAYGARAFRAAW--
                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001123; LysE. Pfam; PF01810; LysE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Best Local Similarity
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01-MAR-2002
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Q8ZHH6
                                                                                                                                                                                                                                                                               RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 APIVLDIMRWGGIAYILWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 RNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYG-DTGRWIFAAG 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                              7 FITGLLLGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S YFQGLALGAAMILPLGPQNAFVWNQGIRRQYHIMIALLCAISDIVLICAGIFGGSALAMQ 64
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STRAIN=24577 / ATCC 700930 / Serotype 2a;
MEDLINE=2559074; PubMed=12704152;
MEDLINE=2590274; PubMed=12704152;
Med. J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Med. J., Acloberg M.P., Plunkett G. III, Rose D.J., Darling A.,
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.,
"Complete genome sequence and comparative genomics of Shigella
flexareri serotype 2a strain 24577:";
Infect. Immun. 71:2775-2786 (2003).
EMBL, AE016988; AAP18212.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                28.8%; Score 343; DB 16; Length 211; 35.2%; Pred. No. 5.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 AFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sest Local Similarity 35.2%; Pred. No. 5.7e-22; Matches 80; Conservative 37; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 211 AA; 23201 MW; 4422D078B182266C CRC64;
                                                                                                                                                                                                                                                                                                     211 AA; 23202 MW; 4422D078B182266C CRC64;
                                                            GO; GO: 0016021; C:integral to membrane; IEA.
GO; GO: 0005233; F:lysine permease activity; IEA.
GO; GO: 0006865; P:lysine permease activity; IEA.
GO; GO: 0006865; P:amino acid transport; IEA.
InterPro; IPR001203; Lipoyl BS.
InterPro; IPR00123; LysE.
InterPro; IPR00123; LysE.
InterPro; IPR00123; LysE.
Pfam; Pf01810; LysE; 1.
Pfam; Pf01810; LysE; 1.
PROSTITE; PS00189; LIPOYL; 1.
Complete protecome.
SEQUENCE 211 AA; 23202 MW; 4422D078B182266C CRCG
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Last annotation update)
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PIR; E85948; E85948
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Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CO-92 / Biovar Orientalis;

MEDLINE=21470413; PubMed=11586360;

Parkhill J., Wheren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Fellwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,

"Genome sequence of Yersinia pestis, the causative agent of plague.",
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33.1%; Pred. No. 2.7e-21;
" wiematches 70; Indels 48; Gaps
                                                                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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HIGSRAMB; TIGR00498; 2a75; 1.
HIGHDCAMB: TIGROCEIN; Complete proteome.
SEQUENCE 205 AA; 22164 MW; 2969524391474CDA CRC64;
ol-uum-2003 (TrEMBLrel. 24, Last annotation update)
Putative LysE type translocator (Hypothetical protein).
YPO0918 OR Y3305.
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60; 60:0006253; F:lysine permease activity; IEA.
60; 60:0006865; P:amino acid transport; IEA.
70:0006865; P:amino acid transport; IEA.
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J. Bacteriol. 1844460114611(2002).
EMBL; AJ414145; CAC89762.1; ---
EMBL; AR013931; AAM66855.1; --
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Matches 80; Conserval
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200 AA.

PRT;

PRELIMINARY;

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Q9HW36 ID Q91 AC Q91

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67 APIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 FITGLLLGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNA 66
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                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 15592 / PAO1;
STRAIN=ATCC 15592 / PAO1;
SEDINGE 204373737, PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Polger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 200;
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GO; GO: 0016020; C:membrane; IEA.
GO; GO: 0005489; F:electron transporter activity; IEA.
GO; GO: 0005293; F:lysine permease activity; IEA.
GO; GO: 0006865; P:amino acid transport; IEA.
GO; GO: 0006118; P:electron transport; IEA.
InterPro; IPR002109; Glutaredoxin.
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Pred. No. 4.8e-21;
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PROSITE; PS00195; GLUTAREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE004852; AAG07753.1; -. PIR; D83100; D83100.
                                                                                                                                                     Bacteria; Proteobacteria; Gamm
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
hes 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                             Pseudomonas aeruginosa.
                                                                          Probable transporter
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STRAIN=A3(2);
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LysE family transporter.
LYSE OR ATU0927 OR AGR_C_1690.
Kanthomonadaceae; Xanthomonas.
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Matches 69; Conserv
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01-JUN-2003
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cromin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                           "A set of ordered cosmitors and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
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Nature 417:141-147(2002).

Nature 417:141-147(2002).

Substituting AL939131; CAB93746.1; -
GO, GO:0016020; Camenbrane; IEA.
GO; GO:0016029; F:lysine permease activity; IEA.
GO; GO:0005293; F:lysine permease activity; IEA.
InterPro; IPR001123; LysE.
Pfam; PF01810; LysE; 1.
Complete proteome.
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                          MEDLINE-97000351; PubMed-8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81; Indels
                                                                                                                                STRAIN-A3(2);
Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 SLIWPPLVGFGAALSRPLSSPKVWRWINVVVAVVMTALAIKLM 233
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 AA; 20686 MW; DD1BD686CCC04DA1 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.6%; Score 328.5; 34.8%; Pred. No. 1e-
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Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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ESEQUENCE FROW N.A.

STRAIN-306 / ATCC 13902 / XV 101;

MEDLINE-2202145; PubMed=12024217;

Ad Silva A.C.R., Ferro D.A., Relnach F.C., Farah C.S., Furlan L.R.,

Ad Silva A.C.R., Ferro D.A., Relnach F.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Alves L.M.C., Cannavan F., Cardoxo J., Chambergo F., Ciapina L.P.,

Cicarelli R.M.B., Coutnino L.L., Cursino-Santos J.R., El-Dorry H.,

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Kacuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Locali E.C., Machado M.A., Madeira A.M.B.N., Martinaz-Rossi N.M.,

Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V. K., Oliveira M.C., Oliveira V.R.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Trindade dos Santos M., Triffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.;

Whore specificities.',

Nature 41745944312021.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 LISNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 VATDIRNRVRVEVSVDKQRVWVKPMLMAIVLIWLNPNAYLDAFVFIGGVGAQYGDIGRWI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VIMEIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVD
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Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Worura V.K., Zhou Y., Chen L., Nood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 FAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.5%; Score 328; DB 16; Length 208; 29.6%; Pred. No. 1.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 AA; 22323 MW; 614712E91CEF2BB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 21, Last sequence update) (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE011957; AAM37978.1; -...
GO; GO:0016020; C:membrane; IEA.
GO; GO:000593; F:lysine permease activity;
GO; GO:0006865; P:amino acid transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 APIVLDIMRWGGIAYILLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 YLNGMLVAFGLIMAIGAQNAFVLAQSLRREHHLPVAALCIVCDAILVAAGVFGLATVLAH 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 FITGLLLGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 NPTLLAIARWGGAVFLIWYGAKALRSACSK-----QSLQHQQ------GQGV----
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I., Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moszcaz A., Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stiepandic D., Hoheisel J., Straetz M., Helm S., Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B., Fraeer C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 FAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKUM 233
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                                                                                                                                                                                                                  "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Brviron. Microbiol. 4:799-808 (2002).

EMBL, AE01677; AAN6541.1; -.

TIGR; PP016177; AAN6541.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:000520; F:lyshine permease activity; IEA.

InterPro; IPR001123; LysB.

Pfam; PF01810; LysB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 27.1%; Score 323; DB 16; Length 20
1. Similarity 32.2%; Pred. No. 3e-20;
73; Conservative 47; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 AA; 21665 MW; 724CFB7366E2B12F CRC64;
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Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Ls
01-JUN-2003 (TrEMBLrel. 24, Ls
Membrane transport protein.
YGGA OR XCC2954.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome
SEQUENCE 204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=340;
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оврега;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 TDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFA 183
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                                                                                                                                                                                                                                                                                                                                                      MEDLINE=2160851; PubMed=11743194; Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Mollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.; Cielo C., Strub G., Cielo C., Slater S.; Strub G., Celo C., Slater S.; Strub G., Celo C., Slater S.; Strub G., Schen Sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens CS8."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.4%; Score 326.5; DB 16; Length 202;
31.6%; Pred. No. 1.5e-20;
ive 42; Mismatches 83; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 MEIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL
                                                                                                                                                                                                                               "The genome of the natural genetic engineer Agrobacterium tumefaciens
   Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.
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Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
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Pseudomonadaceae; Pseudomonas.
NCBL TaxID=160488;
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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GO: GO:0005293; F:lysine permease activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
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                                                                                                                                                                                                                                                                                                Science 294:2317-2323(2001).
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les 73; Conservative
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62 LLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSA 121
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                                                                                                                                                                                                                                                                                       2 VIMEIFITGLLIGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLLSDVFLFIAGTLGVD 61
"Comparison of the genomes of two Xanthomonas pathogens with differing host specificities."

Mature 417-455-463 (2002).

BMBL, AB012410; AM44226.1; -.

GO; GO:016020; C:membrane; IEA.

GO; GO:000523; F:lysine permease activity; IEA.

GO; GO:0006865; P:maino acid transport; IEA.

InterPro; IPR001123; LysE.

Complete proteon.

SEQUENCE 208 AA; 22266 MW; 8A1306B919A01029 CRC64;
                                                                                                                                                                                                  Query Match
25.9%; Score 309; DB 16; Length 208;
Best Local Similarity 28.8%; Pred. No. 5.1e-19;
Matches 67; Conservative 44; Mismatches 90; Indels 32; Gaps
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Search completed: March 12, 2004, 18:26:16 Job time : 48 secs

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OM nucleic - nucleic search, using sw model	<pre>March 15, 2004, 10:15:20 ; Search time 9505 Seconds (without alignments) 10825.501 Million cell updates/sec</pre>	US-09-105-117K-3 2374 1 agatactcctttggaagaaagtaacaccttcagcaaatgg 2374
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6940544 3470272 seqs, 21671516995 residues Total number of hits satisfying chosen parameters: IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 gummaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

gb htg: *
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	ult No.	Score	Query Match	Length	DB	ID OI	Description
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	44	111.2	4.7	10278		AE015317	AE015317 Shigella
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BCT 19-MAR-2001 $\mathring{\mathbf{L}}$ Lijic,M., Sahm,H. and Eggeling,L. A new type of transporter with a new type of transporter with lysE gene; lysG gene; Lysine export regulator protein; Lysine exporter protein; Lysine governor.
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacterium. linear DNA CGLYSEG 2374 bp C.glutamicum lysE and lysG genes. X96471.1 GI:1729753 RESULT 1 CGLYSEG/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

ALIGNMENTS

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                                                                                        Vrljić,M.M.
Direct Submission
Submitted (07-MAR-11996) M.M. Vrljic, Institut fuer Biotechnologie
Submitted (07-MAR-11M Juelich, Postfach 1913, D-52425 Juelich, FRG
1, Forschungszentrum Juelich, Postfach 1913, D-52425 Juelich, FRG
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Mol. Microbiol. 22 (5), 815-826 (1996)
97126810
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| trans1 table=11
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                     'note="Lysine governor"
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complement(82..954)
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complement(82..954)
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1025. .1726
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/gene="lysE"
1025. .1726
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                                                                              (bases 1 to 2374)
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JOURNAL
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CAACAACTIGGAGTTTTCTGACGCCGAGTTGGAGGCGATCGATGAGATTTCCCACGACGC CAACAACTIGGAGGTTTTCTGACGCCGAGTTGGAGGCGATCGATGAGATTTCCCACGACGC CGGCATCAACATTTGGGCGAGAGGCCACCGATTCCAAAACCCGCGAAAACTAACCCATCAA CGGCATCAACATTTGGGCGAAGGCCACCGATTCCAAAACCCGCGAAAACTAACCCATCAA CATCACTTTGATGGGCGTAATCACAACTGCCACGACGACGAAAACTAACCGATCAA CATCACTTTGATGGCCAATGCGGTAATCACAACTGCCACGACGACGACGACGACGACGAAACTAACCGATCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAAACTGAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAAAAAAA	1654 CACCTTGGGGCTGGAACGGGCGGGGAAAATGCTGCTGCGCGGAAACCCAGCGGGAA 1595	901 GGTCAGCACTGACATCAACATGAGCTTTACCCAAACCGCTGCTTATCGAGGCTCAC 960		1141	1114 1321 1054 1381 994	934 CACTTTGCTCTCAATCATGATGAAGGCAGCTTCGAAGGCGCCTCCTTAGCCCTTTCCAT 1501 TTCCCCCTCGGCGGTGAGTCAGCGCTTAAAAGCTCTCGAGCATCACTGGCCTTTCCAT 874 TTCCCCTTGGCGCGGTGAGTCAGCGCGTTAAAGCTCTCGAGCATCACGTGGGTGTT 1561 GGTATCGCGCACCCAACGGCGCTAAAGCTCTCGAGCAAGCGGGTGAAGTGTT 1561 GGTATCGCGCACCCAACGGCCAAAGCAAGCGAAGCGGCAAGCAA

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PWANYRHVWLI AMSAVLWHTSTTTDYLSALHVVI PPLAMGTVRLSVWTVDVMKEVERS
RELEASLRVTERLRPAQELHDTI GQHLAAMSVKSRLALALAKRGDDRLENBI RELQK
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LVREATTNILRHSDATDATLTLSSTEVRMDNNGVNKDIGRLSGLSALRSRAESAGMTL
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histidine kinases"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="PP00072:Response regulator receiver domain
PP00196:Bacterial regulatory proteins, luxR family"
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WALGITVIVLLAALSLFRSMCSIASKDVQGKVISKGKRGLVTGRATVIGGVMGLVAGL
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AALKOKKARRRVILSKBMIUVTALSTAFTABSGOSISIOSLGFFILTASGLASWYGG
RISGIWSDHSSRVWARGALFGSIULILIVULSSAPPAQINTLUFPLSFILTLÄHTA
IRVARKITVWDMAEGDQRTRYVADANTLMGVULLIUGALSGFIAIFGAALLFILAHT
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3063. .3983
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/note="Pg00005.ABC transporter
TIGR009661:a0501s02: Type II (General) Secretory Pathway
(IISP) Family protein
TIGR00968:3a0106801: sulfate transport system permease
Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida,
Tokyo 194-8533, Japan (B-mail: Banakagawa@xanagen.com,
Tel:81-44-8629-3031, Fax:81-44-813-1651)
This sequence is conducted by collaboration of Kyowa Hakko Kogyo
Co. Ltd. And Kitasato University.
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TIGR01166:cbiO: cobalt transport protein ATP-binding
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/gnee=(Gg10945"
/codon_start=1
/transI_table=11
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/gene="Cg10944"
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FIJVIVPRSTLEHGRILLAFURADI FEGTLRSNISMHEDNVPIDPQVIRASGLTDI
IEVDGLDAPVRDTGSNLSGGGRORVALARALHADAEVLVLMDPTSAVDSVTEVSIAQG
IKQLRAGKTITVSSSPAPVILADRVISHV"
                                                                                                                                                                                APIAEPLHLTNVLSFLTDRFMPINIWVRFPVIVGVLIMFVATLYYMAPNARFWKFRML
SLOSFRAIVGTILAGVGLMFYFTLFAAFSSYGAVGSLLAVFTALWYPNICLIIGLKID
VEISRAKQLQAGMPAEDYSLVPPRSIEKVAKWKQRQQRLMDQAAAIREESN"
8672. . 1011
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GLIVDHAYLTKDLRRLWOGLVAFVVLFVVLSFSYRRGSSALMRAVWFESHALRYBVAD
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PF00664:ABC transporter transmembrane region."
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/gene="Cg10953"
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ETEPTVPDDTPLGGSAVATDTRNRVRVEVSVDKQRVWVKPMLMALVLTWLNPNAYLDA
FVPIGGVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVV
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corprobacterium glutamicum genes encoding metabolic pathway
proceins
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/note="unnamed protein product; RXA01394"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Corynebacterium glutamicum"
/wol_type="unassigned DNA"
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                                                                                                                                                                                                                        DNA
                                                                                             GTTGATGCAGCAATCGAGGGATTGCGGCCT 2290
                                                                                                                GTTGATGCAGCAATCGAGGGATTGCGGCCT 870
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BASF AKTIENGESELLSCHAFT (DE)
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Sequence 53 from Patent W00100843.
AX063771
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AX063771/c
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04,C12P13/08,
C12P19/00,C12P19/34,C12P21/02,C12Q1/37,C12Q1/68,G01N33/53, PC
                                                G01N33/569,G01N33/68,G01N37/00//C12P21/08,(C12N1/21,C12R1:15),
(C12N1/21,C12R1:13),(C12N1/21,C12R1:01),(C12P13/08,C12R1:15),
C12N1S/00,C12N1S/00
C12NS/00,C12N1S/00
Novel polymucleotide
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/organism='Corynebacterium glutamicum'
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100.0%; Pred. No. 9.5e-
...tive 0; Mismatches
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/organism="unidentified"
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Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 629 GATTCCAAAACCGGGAAAACTAACCCATCAACATCAGTTTGATGGGGTCATC 688 Db 822 GATTCCAAAACCGGGAAAACTAACCCATCAACATCAGTTTGATGGGCAAAGGGGTCATC 763	Oy 689 ACAACTGCCACGACGTTGATCCAGGGCCACACCTTGGGGCTGGACAGGGGGGGAC 748	Oy 749 AATGCTGCGCGAAACCCACCAGGGGAACCAGATCAGGTTGCGGGGAACGCGCA 808 Db 702 AATGCTGCGCGAAACCCACCAGGGAACCAGATCAGGCTTGCCGCGAACGCGCA 643	QY 809 GOGGGBAAATCTACCGTCCGTCTCGCCGTATTGCGCGCCGCCGCCGCCGATAAACACA. 868 AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA AA	942 GOGGGGGGGAAAALCCACOGLCGGGGGGGGGGGGGGGGGG	929 TITRACCAAACCGCTGCTTATCGACGCTCACCCGCACCCGGTTGCGCGTTGCTCACCCGCTCACCGGTTGCGCGGTTGCTCACCTCACCCGCACCCGGTTGCGCGGTTGCTCACCTCACCTCCACCCCGGACCCGGTTGCGCGGTTGTCACCACCTCCACCCCGGACCGGTTGCGGTTGTCACCACCTCCACCCCGGACCGGTTGCACCTCCACCCCGGATCGGGTTGTCACCACCTCACCCCGGATCGGGTTGTCACCACCTCACCACCGGTTGCACCTCACCACCGGTTGCACCTCACCACCGGTTGCACCTCACCACCGGTTGCACCTCACCACCGGTTGCACCTCACCACCGGTTGCACCTCACCACCGGTTGCACCTCACCACCAGTTCACCACCTGCACCACCAGTTCACCACCACCACCACACCACTCACCACCACACACA	QY 989 GIGGCGCCGAACCGCCCAAAGGCGTCATCAGGCACGCTTGCTT	Oy 1049 AIGATCIGIGGCGCTTCCACCTTGTTTGTCARGGGGTCTTTGGCTGCCATGACGCAAAC 1108 Db 402 AIGATCIGIGGCGCTTCCACCTTGTTTGTCARGGCGTCTTTGGCTGCCATGACGGCAAAC 343	Qy 1109 CATAACAGGTAAGCGATGCCACCCCAGGCATAATATCGAGCACGATCGGCGGGCATTG 1168	QY 1169 GACAAAAGATCAACGCCCAAGGTGCCGGCGATGAAAAAGACGTCAGAAATTAAACAC 1228	QY 1229 ACGAGAAGAACGCGAATGAGTCCTTCGCGCTTAATTCCTTGTTTAATCACCAGTACATTC 1288	Oy 1289 TGCGGTCCGATGGACACATAAAGACTCGCCCCCAAAAGGACCTGTAATGAAGATTTCC 1348	OY 1349 ANGATCACCATGGTGACCTATGGAAGTACTTAAGTAAAATGATTGGTTCTTAAGGTT 1408 Db 102 ATGATCACCATGGTGACTAAGAAGTACTTAAGTAAATGATTGGTTGTTAAGATGATTAAGATGATTGATGA		RESULT 11 AP005218 LOCUS DNA linear BCT 10-JUL-2003 DEFINITION Corynebacterium efficiens YS-314 DNA, complete genome, section		SOURCE Corynebacterium efficiens YS-314 ORGANISM Corynebacterium efficiens XS-314 Bacteria, Actinobacteridae, Actinomycetales,	
989 GTGGCCACCGCCGAACGCCCAAAGGCGTGTCATCGGGCACGGTTGGTT	1049 ATGATCTGTGGGGCTTCACCTTGTTGTCATGGCGTCTTTCGCTGCCATGACGCAAAC	Dy 1109 CATAACAGGTAAGCGATCCCAGGGCATAAATGTGAGGAGATTG 1168	Cy 1169 GACAAAGATCAACGCCCAAGGTGCCGGCGATGAACAAAAAGACGTCAGAAATTAAACAC 1228 Db 282 GACAAAAGATCAACGCCCAAGGTGCCGGTGAACAAAAAAGACGTCAGAAATTAAACAC 223	Oy 1229 ACGAGAAGAACGCAATGAGTCCTTCGCGCTTAATTCCTTGTTTAATCACCAGTACATTC 1286	QY 1289 TGCGGTCCGATGGACAGTAAAAGACTGGCCCCCAAAAGCAGACCTGTAATGAAGATTTCC 1348 Db 162 TGCGGTCCGATGGACAGTAAAAGACTGGCCCCCCAAAAGCAGACCTGTAATGAAGATTTCC 103	1349 ATGATCACCATCGTGACTATGGAAGTACTTAAGTAAAAAGA;	OY 1409 TAMTARCTICATCAACTGGAACTTTGTC 1450	Ξ		-	REFERENCE 1 AUTHORS 1 AUTHORS Kim, J. W., Kroeger, B., Schroeder, H., Zelder, O., Haberhauer, G., Kim, J. W., Lee, H. S. and Hwang, B.J. TITLE Corynebacterium glutamicum genes encoding metabolic pathway	DOURNAL PAtent: WO 0166573-A 51 13-SEP-2001; BASF ATIENGESELLSCHAFT (DE) FEATURES LOCAtion/Onalifier	<pre>source 1 .822 /organism="Corynebacterium glutamicum" /mol type="unassigned DNA" /db.xrefe="eaxon:1718"</pre>	CDS 101802 /note="unnamed protein product; RXA01394" /codon start=1 /transI_table=11 /protein_id=456988508.1" /db xref="d1:188518"	/db_xref="REMTREMBL:CAC88508" /translation="WBIFITGLIGASILLS:OPQNVLVIKQGIKBEGLIAVLLVCLI SDVFLFIAGTGVDLLSNAAPIVLDINRWGGIRYLWFAVWAAKDAMTNKVBAPQIIE FTREPVPDFDFFRESAVAFVRVEVSVDKORVWYPMIMAIVITMINPAYLLDA	FVFIGGVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAALSRPLSSPKVWRWINVVV AVVMTALAIKLMLMG" ORIGIN	Query Match 34.6%; Score 822; DB 6; Length 822; Best Local Similarity 100.0%; Pred. No. 6.1e-191;

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complement (2513 . 3271)
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hote="CE1185, similar to AE007003-6|AAK45530.1| percent
identity: 60 in 155 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (3282. .3836)
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transI table=11
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                                                          Comparative Complete Genome Sequence Analysis of the Amino Acid
Replacements Responsible for the Thermostability of Corynebacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamura, Y., Ikeo, K., Suzuki, M. and Mashima, J. are at the National Institute of Genetics, Mishima, Shizuoka, 411-8540 Japan Itoh, T. is at the Japan Biological Information Research Center, Koto-ku, Tokyo, 135-0064 Japan Yamagishi, A. is at Tokyo University of Pharmacy and Life Science, Hachioji, Tokyo, 192-0392 Japan Inc., Kawasaki, Kanagawa, 210-8681 Japan Inc., Kawasaki, Kanagawa, 210-8681 Japan The other authors are at the National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       774. .1271
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                                                                                                                                                                                                                                                                                                                                                            Submitted (17-MAY-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:biodemite-go-ip, Tel:81-3-3481-1933, Fax:81-3-3481-8424) Kawarabayasi, Y is officially affiliated with the National Institute of Advanced Industrial Science and Technology, Tsukuba, Ibaraki, 305-8566 Japan
Sugimoto, S., Matsui, K., Yamagishi, A., Kikuchi, H., Ikeo, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Corynebacterium efficiens YS-314"
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Kawarabayasi,Y., Yamazaki,J., Hino,Y., Kikuchi,H. and
Director-General of Biotechnology Center.
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Location/Qualifiers
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AUTHORS
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vccadyatysqdrvwtrngyrhrdfdtrygtidvavpklrtgsffpdwilerrtrar
alttylatcylkgystrrwndlvatlginnlsksqysdwakdidQmyeefrtreldtg
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DLKARGLMEVYLVTSDAHLGTQHAIGEVLPNASWQRCRTHFSKNLYGMVSKTQMPTLS
AMFHTIFQQPDAQSVWGQAREVVAFCEQKFPDVADYLEEALDELLAETNAFKSVWTKV
WSNNPTERLNREIRRRTDVVGIFPNRDAVVRLVGAVLAEQHDDMIQQKRYMSLTSLEQ
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LILLAFGFSLATWARDRGEVEWPYVGWSLLGRIPGSVLGTWAVVAMPYARPAGKIKIVLATAV
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VCFVIGSALISTALIYGAGALGWMHLQAALVYAPAVIAGYFLSGVVNKHLNRRLIFLGS
VTISLIGSGMVITQAAGIF"
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/translation="MMPIHLDTLLTIIDEGSFENASLALSISPSAVSQRIKALEKSVG
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FPPPVREXVAHWAAVTLTLRVUBDEAHTLSLLARGSVLGAVTRADPPVRGSTVLEGVNR
HLPVATPELRARYTVDGQPDWVRMPVLRFGPNDVLQDRDLEGRVDGAVARRYSVVPS
TDAVVDAARAGLGGGGGAAPMLAABGAAPMLAAGDVVQLDERVVDTPLYWQRWRLESRLLARI
TDAVVDAARAGLRT"
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                                                                       CTAAAAAGCAGGAGAAAGTGATCCTCCTCGATGAGATACCCATTGACACACCGATGTATTGG
                                                                                                                                                                                                                                                                  CAACGATGGCGCCTGGAATCTAGATCTCTAGCTAGACTCACAGACGCCGTCGTTGATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium efficiens lysG, lysE genes for Lysine export transcriptional regulatory protein, Lysine exporter protein, complete cds.
AB083133
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( Chaese 1 to 1771)
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/mol_type="genomic DNA"
/db_xref="taxon:152794"
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/transl_table=11
/product="Lysline exporter protein"
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/db_xref="GI:20065740"
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complement(47..919)
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/translation="wisspilketdsvyllamdkhyvstdlyvsvpqqqptaligpwdc
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TRANSPYVLLDBPTYLLDVAHQYQLLELANALAYGQLGRTYTYHDLGQAVRYADHLIWK
GGAVYAEGAPSIMTPQLISEVPDINVDVHTIDDHVVIVPKTMPQQPDVSVLENLQ"
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/note="HAMPEam hit to PF01910, Protein of unknown function
DUF77"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MLIDMILAFSVAPTETPNNKAEMADVVAEAIRVVRESGLPNETN
AMFTLIEGEWDEVMAVVKKATDAVLAVSPRASLVIKADIRPGYTGQLQQKVASVERVL
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//locus fage*DIP1058"
//locus fage*DIP1058
11.0 kDa protein Rv1898 or WT1949 or WTCY180.20c
11.0 kDa protein Rv1898 or WT1949 wrcytu (007734) (102 aa) fasta scores: E():
5.8e-16, 56.43% id in 101 aa, and to Aquifex aeolicus hypothetical 17.9 kDa protein AQ_2067 TR:067847
(EMBI:ABG00771) (157 aa) fasta scores: E(): 4.7e-08, (0.19% id in 102 aa"
                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (03-OCT-2003) Cerdeno-Tarraga A.M., submitted on behalf
of the Pathogen Sequencing Unit, Sanger Institute, Wellcome Trust
Genome Campus, Hinxton, Cambridge CB10 1SA E-mail:
Whitehead, S. and Barrell B.G. Parkhill, J. The complete genome sequence and analysis of Corynebacterium diphtheriae NCTC13129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (405. .4762)
/note="Putative iron uptake system. Low GC content
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APP-binding component"
/protein_id="CAE49580.1"
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/product="Conserved hypothetical protein"
/protein_id="CAE49578.1"
/db_xref="G1:38199913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .349535
|organism="Corynebacterium diphtheriae"
|/mol_type="genomic_DNA"
|errain="NCTC13129"
                                                                                                                                       Nucleic Acids Res. 31 (22), 6516-6523 (2003)
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/locus_tag="DIP1059"
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complement".
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/note="biotype gravis"
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/locus tag="DIP1058"
76. .402
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                                                                                                                                                                                                                                                                               Cerdeno-Tarraga, A.M.
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ALRHYGDPTNSHIIWGRRIPRTLIAIAAGGASLSLAGVLIQALTRNPLADTGVFGTINAG
AAFTIVIGIALAGSLGSHISIFALAALIGAHILAGATGAACTAALANSGKGSDPLRLVLAGVAL
SALITGIGGLSLVARDELKSWWGWIDAGSYQPAVAGVGLILGIILYTATCMRC
INALSGLGDELTTWGASLAKTRLFFFFALVULAAASHTAAAGVITFLGLMVPHIARMIV
GPNLIRLVATASLIGPIIUULSADILGRIITVEGFFFARAAGVITFLGLMVPHIARMIV
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/note="Signal peptide predicted for DIPI061 by SignalP 2.0
|MPW (Signal peptide probability 1.000) with cleavage site
probability 0.663 between residues 34 and 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 AATTCCAGAGGGTTCCCGCCGCCAGCCAGGGTAAGTCCCTGTCTGAGGGCATGTTGAACGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 TGCGCAGATGGCGCTTGCATGGTGCTGCGGAGCAAGGAGAGAGTACGGCGCGGATACCGT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTTACGTGGGTATTTCTTCCTACGGTCCAGAGCTCACAGCGGAGGCGGCTGAGTTCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus_tag="DIPL062"
/note="Similar to Escherichia coli iron(III)
dicitrate-binding periplasmic protein precursor FecB or
B4290 SW.FECB_ECOLI (PIS028) (300 aa) fasta scores: E():
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /noce="myneta" int to PF01032, FecCD transport family" order (complement (3096. .3161), complement (2934. .2990), complement (2838. .2903), complement (2670. .27831), complement (2670. .2785), complement (2674. .2609), complement (2394. .2459), complement (2211. .2276)) /locus_tag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag="mynetag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=\overline{\phantom{a}}9 probable transmembrane helices predicted for DIP1061 by TMHMM2.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
product="Putative iron-siderophore uptake system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 349535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="BlastProDom hit to PD001557, PD001557"
complement(2205. .3095)
/locus_tag="DIP1061"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 724.4; DB 1;
Pred. No. 1.2e-166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 931;
                                      transmembrane component"
/protein_id="CAE49584.1"
/db_xref="GI:38199916"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signal-peptide site"
complement (2199. 2525)
/locus_tag="DIP1061"
                                                                                                                                                                                                                                                                                                                                                                                                         complement (3090. .3191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus_tag="DIP1062"
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58.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Signal peptide predicted for DIP1060 by SignalP 2.0 HMM (Signal peptide probability 0.966) with cleavage site probability 0.180 between residues 25 and 26; signal-peptide site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=Figuriar to Streptomyces coelicolor putative iron-siderophore uptake system transmembrane component sci51.26C TR:098214 (EMBL.AL10984B) (375 aa) fasta scores: E(): 5e-40, 40.74 id in 324 aa, and to Escherinia coliferric enterobactin transport system permease protein fepg fepg or B0589 SW:FEPG ECOLI (P23877) (330 aa) fasta scores: E(): 1.8e-45, 44.09% id in 322 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TALSAASWGAGSLNGIRWTIAIPACCYIAILITTTIPLERFLDVLSLGDDLAVGLGIR
LQITKLLLLVGGVFLVAATTAVAGPIAFVALASPHIARALITSSARTPLVETSVIGALL
IIVADLIGQRLFYPTQLPVGLVTVTIGGMYLLWLIARGSKENS"
complement (2108. . 2182)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="NRALVILSSILLVTAAYSLVIPGAGLSTWQLLTSETPLAHTVVW
QWRLPRVVTGIIVGAALAIAGSLFQSLTRNPLGSPDIIGFSTGAYTGVIAAFLLGWSG
FGATIVGALIGGLAVSVVVIALSVRTRIDGLRIILVGLGISAMLSALMRWLITRGELD
                                                                                                                                                                                                                                 /locus tag="DIP1059"
/note="ScanRegExp hit to PS00211, ABC transporters family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus tag="DIP1060"
/locus tag="DIP1060"
/noce="HMMPEam hit to PF01032, FecCD transport family"
order(complement(2105.2161), complement(1979.2044),
complement(1883.1393), complement(1805.1870),
complement(1718.1733), complement(1607.1657),
complement(1445.1510), complement(1319.1384),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus tag="DIPI059"
/note="ScanRegExp hit to PS00017, ATP/GTP-binding site
motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus_tag="DIP1060"
/note="9 proble transmembrane helices predicted for
DIP1060 by TWHAMM2.0"
complement(1250. .1564)
                                             complement (579. .797)
/locus tag="DIP1059"
/note="ProfileScan hit to PS50100, 2nd half motif for nucleotide binding, associated with P-loop."
complement (753. .797)
                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="DIP1059"
//note="Profilescent hit to PS50101, P-loop nucleotide
binding motif (does not find all)."
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/locus_tag="DIP1061"
/note="Similar to Streptomyces coelicolor putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transI_table=11
product="Putative iron-siderophore uptake system
               note="HMMPfam hit to PF00005, ABC transporter"
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/protein_id="CAE49582.1"
/db_xref="G1:38199915"
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'note="Blact"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (1223. .2182)
/locus_tag="DIP1060"
complement (1223. .2182)
/locus_tag="DIP1060"
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                                                                                                                                                                                                                                                                                                                                                complement (1047. .1124)
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trans table=
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
Novel polynuclectides
Patent: EP 1108790-A 3455 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
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|organism="Corynebacterium glutamicum"
|mol_type="unassigned DNA"
|db_xref="taxon:1718"
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ilarity 100.0%; Pred. No. 6.5e-163;
Conservative 0; Mismatches 0;
Sequence 3455 from Patent EP1108790.
AX123539
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/db_xref="G1:28550159"
/db_xref="RBWTRNBHB.:CAD67811"
/translation=mVIMERETFGILLGSIGPQNVLVIXQGIKREGLIAVLLV
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IIEETEPTVPDDTPTGGGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLIFWLNPNAY
IIEETEPTVPDGTPGGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLIFWLNPNAY
IIDAFVFIGGVGQQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSFPKVRWIN
VVVAVVWTPLAIKLMLMG"
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Increasing microbial production of amino acids, especially lysine - by improving export carrier activity or corresponding gene expression, also new export and regulatory genes from Corynebacterium.
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                                                                                                                                                                                                                                                                                                                                         DNA encoding LysG, LysE and ORF3 from Corynebacterium glutamicum.
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This DNA, isolated from Corynebacterium glutamicum, contains the LysG, LysE and ORPS genes. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) are oracled into the culture medium. Export of (A) has been found to depend on a single gene. NB. This sequence has been created from the information given in table 2 of the specification.	Ouery Match Best Local Similarity 100.0%; Score 2374; DB 2; Length 2374; Best Local Similarity 100.0%; Pred. No. 0; Matches 2374; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 2374; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 AGATACTCCTTTGGAAGAAACCATGACGCATGCGTGACATTGTTGCGTCTGGAAAGGC 60	GGTGGAGGAACGGGGATGACGGTGAAACTTGTTGCACGGGCGACGACGAGGGGGGGG	2014 GAACHATTGAIRTGAIRTGAIRTGAIRTGAIRTGAIRTGAIRTGA
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1740 1620 GCGCGGATGTGAAGTAGTAGAACTTGGAACCATGCGCCACTTGGCATTGCAACCCC 1920 1140 1115 1055 1440 1500 1680 1475 CITITCGCIGCCATGACGAAACCATAACAGGIAAGCGATGCCACCCCACGCGAT 1235 AAAAGACGTCAGAAATTAAACACACGGGAAAGAACCGCAATGAGTCCTTCGCGCTT 1260 CTTGTTTAATCACCAGTACATTCTGCGGTCCGATGGACAGTAAAAAGACTGGCCCC 1320 AGCAGACCTGTAATGAAGATTTCCATGATCACCATCGTGACCTATGGAAGTACTTA 1380 CCTCGGCGGTGAGTCAGCGCGTTAAAGCTCTCGAGCATCACGTGGGTCGAGTGTT 1560 635 935 815 755 960 AAAATGGTGTGCTGCAAGCAGAACTAAAGGCGCAACTATCTGGACGCCTTGCTGA rcececanceancegeccanageanceangegegegegeneangergege TTATCCTTGCTGCGCGTGGAGATGTTTTAGGAGCGGTAACCCGTGAAGCTAATCC CGTTAACCATCGCCATCAACGCAGATTCGCTATCCACATGGTTTCCTCCCGTGTT CTTGTTTAATCACCAGTACATTCTGCGGTCCGATGGACAGTAAAAGACTGGCCCC TECTCTCAATCATTGAAGGCAGCTTCGAAGGCGCCTCCTTAGCCCTTTCCAT AAATGGTGTTGCTGCAAGCAGAAACTAAAGGGCAACTATCTGGACGCCTTGCTGA AGGTAGCTTCTTGGGGTGGAGCAACGCTCACGCTGCGCTTGGAAGATGAAGCGCA GCACGATTGCCATCAACATGGGCTTTACCCAAACCCGCTGCTTATCGACGCTCAC CCCGCACCCGGTTGCGCGTGTCAGTGGCCACCGCCGAACCGCCCAAAGGCGTGTC CTTTCGCTGCCATGACGCAAACCATAACAGGTAAGCGATGCCACCCCAGCGCAT CGAGCACGATCGGCGCGCCATTGGACAAAAGATCAACGCCCAAGGTGCCGGCGAT

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2374 AGATACTCCTTTGGAAGAAACCATGTACGCATTGCGTGACATTGTTGCGTCTGGAAAGGC 2315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for producing L-arginine in a microorganism (e.g. coxymeform bacteria) that has L-arginine producing ability and has been modified for enhanced expression of the lysE gene. The microorganism is also modified so that an arginine repressor (argR) does not function normally. The method of the invention is useful for the enhanced production of L-arginine which is useful in liver function promoting agents, amino acid infusion and comprehensive amino acid pharmaceuticals. The present sequence represents a DNA fragment containing Corynebacterium glutamicum Lyse and LysE genes. Note: The present sequence is given as SEQ ID No.24 in the Sequence Listing but is referred to as SEQ ID No.25 in the rest of the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACCAGGCATTGATTGGTGCTTCGTCAGTTGAGCAGCTGGACAACAGCCTTTGATTCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2374;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2374 BP; 526 A; 640 C; 648 G; 560 T; 0 U; 0 Other;
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                             4; Page 26-27; 36pp; English.
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                                                                                                                                                     1981 ACGCTTCGGTCCCAAAGATGTGCTTCAAGACCGTGACCTGGACGGGCGCGTCGATGGTCC 2040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTGGCGGGATGTGAAGTAGTAGAACTTGGAACCATGCGCCACTTGGCCATTGCAACCCC 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35
                                                CTCATTGCGGGATGCCTACATGGTTGATGGGAAACTAGATTGGGCTGCGATGCCCGTCTT
                                                                                 CCATTGCGGGGATGCCTACATGGTTGATGGGAAACTAGATTGGGCTGCGATGCCCGTCTT
                                                                                                                                                                                                 394 ACGCTTCGGTCCCAAAGATGTGCTTCAAGACCGTGACCTGGACGGGCGCGTCGATGGTCC
                                                                                                                                                                                                                                                          TGTGGGGCGCAGGCGCGTATCCATTGTCCGGCGGCAAAGGTTTTGGTGAGGCAATTCG
                                                                                                                                                                                                                                                                                                             334 TGTGGGGCGCAGGCGCGTATCCATTGTCCCGTCGGCGGAAGGTTTTGGTGAGGCAATTCG
                                                                                                                                                                                                                                                                                                                                                                 CCGAGGCCTTGGTTGGGGACTTCTTCCCGAAACCCAAGCTGCTCCCATGCTAAAAGCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-arginine production; coryneform bacteria; lysE; arginine argR; liver function promoting agent; amino acid infusion; amino acid pharmaceutical; LysG; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA fragment containing C. glutamicum LysG and LysE genes
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1594 CCAGATCAGGCTTGCCGGAACGCGAAAATCCACCGTCCGGTGTCGCGTA 1535	1321 CAAAAGCAGACCTGTAATGAAGATTTCCATGATCACATCGTGACCTATGGAAGTACTTA 1380

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The present invention provides a number of nucleotide and protein

CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These

are useful for identifying the mutation point of a gene derived from a

cm nutant of coryneform bacterium, measuring expression amount and analysing

CC coryneform bacterium, measuring expression amount and analysing

CC coryneform bacterium, and identifying a homologue of a gene derived from

CC coryneform bacterium, coryneform bacteria are useful for producing amino

CC coryneform bacterium, coryneform bacteria are useful for producing amino

CC acids, nucleic acids, vitamins, saccharides and organic acids amino

CC acids, nucleic acids, vitamins, saccharides and organic acid described

CI nelectronlarly L-lysine. The present sequence is a nucleic acid described

CI nelectronic format directly from the Buropean Patent Office

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from the Buropean Patent Office

CC in electronic format SC 78, 91049 C; 97618 G; 80586 T; 0 U; 0 Other;

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llarity 100.0%; Pred. No. 4.9e-299;
Conservative 0; Mismatches 0;
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129695 CCGAGGCCTTGGTTGGGGACTTCTTCCCGAAACCCAAGCTGCTCCCATGCTAAAAGCAGG 129754
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129455 CGTGGCGGGATGTGAAGTAGTAGAACTTGGAACCATGCGCCACTTGGCCATTGCAACCCC 129514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; vinsamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
                                                                                           CCTGGAATCTAGATCTCTAGCTAGACTCACAGACGCCGTCGTTGATGCAGCAATCGAGGG
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                                         129515 CTCATTGCGGGATGCCTACATGGTTGATGGGAAAACTAGATTGGGCTGCGATGCCCGTCTT
                                                                             1981 ACGCTTCGGTCCCAAAGATGTGCTTCAAGACCGTGACCTGGACGGGCGCGTCGATGGTCC
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AAF11753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP mucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes
                                                                                                                                                                                                                                                                         Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and
Schroeder H, Zelder O, Haberhauer G;
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Length 993;

fine chemical;

(first entry)

Haberhauer G;

Zelder O,

Schroeder H,

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The present invention relates to the isolation of novel Corynebacterium glutamicum genes encoding metabolic pathway (MP) proteins (AAU71863-AAU71922). The metabolic pathway proteins of the invention include enzymes involved in the lyshim actionic biosynthetic pathways. The polymucleotide sequences of the invention can be used for the large-scale production and/or modulation of expression of fine chemicals such as lysine and methionine. The sequences of the invention may be used to identify C. glutamicum and related organisms e.g. C. diphtheriae in a subject to detect diphtheria. AAS96073-AAS96132 represent C. glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding metabolic pathway proteins from Corynebacterium glutamicum, useful for producing methionine and lysine in Corynebacterim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes encoding the novel metabolic pathway proteins of the invention
                                                                                               Metabolic pathway protein; MP; lysine biosynthesis pathway; methionine biosynthesis pathway; large-scale production of Corynebacterium diphtheriae; diphtheria; ds.
                                                                  C. glutamicum gene #21 encoding metabolic pathway protein.
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23-JUN-2000; 2000US-00606740.
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Lee H, Hwang B;
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, Coryneform bacterium and identifying a homologue of a gene derived from acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the Buropean Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 3456; 246pp + Sequence Listing; English.
                                                                                                Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 870 BP; 192 A; 236 C; 245 G; 197 T; 0 U; 0 Other;
                                                                                           Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
(KYOW ) KYOWA HAKKO KOGYO KK
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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80311. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purina and pyrimidine bases, nucleosides, nucleosides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           702 AATGCTGCGCGGAAACCCACCAGCGGGAACCAGATCAGGCTTGCCGCGAACGCGCCA
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99DE-01042087.
99DE-01042088.
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Best Local Similarity 100.0
Watches 822; Conservative
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14-JUL-1999;
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27-AUG-1999;
31-AUG-1999;
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               720
                                                                                                                                       Corynebacterium glutamicum MP protein nucleotide sequence SEQ ID NO:53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; vianin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
                                                                          GGTTTTGGTGAGGAATTGGCCGAGGCCTTGGTTGGGACTTCTTCCCGAAACCCAAGGCT
2021 GACGGGCGCCTCGATGGTCCTGTGGGGCGCAGGCGCGTATCCATTGTCCCGTCGGCGAA
                                                          2081 GGTTTTGGTGAGGCAATTCGCCGAGGCCTTGGTTGGGACTTCTTCCCGAAACCCAAGCT
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99DE-01032126
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Haberhauer G;

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The present invention relates to the isolation of novel Corynebacterium glutamicum genes encoding metabolic pathway (MP) proteins (AAU71863-AAU71922). The metabolic pathway proteins of the invention include enzymes involved in the lysine and methionine biosynthetic pathways. The polymucleotide sequences of the invention can be used for the large-scale production and/or modulation of expression of fine chemicals such as lysine and methionine. The sequences of the invention may be used to identify C. glutamicum and related organisms e.g. C. diphtheriae in a subject to detect diphtheria. AAS96073-AAS96132 represent C. glutamicum genes encoding the novel metabolic pathway proteins of the invention
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                                             Nucleic acids encoding metabolic pathway proteins from Corynebacterium glutamicum, useful for producing methionine and lysine in Corynebacterim and Brevibacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                  629 GATTCCAAAACCCGCGAAAACTAACCCATCAACATCAGTTTGATGGCCAATGCGGTCATC
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                                                                                                            Disclosure; Page 214-215; 316pp; English.
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 2001-582269/65
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methionine biosynthesis pathway; large-scale production of fine chemical;
Corynebacterium diphtheriae; diphtheria; ds.
642 GCGGCGAAAATCCACCGTCCGGTGTCGCCGTATTGCGCGCCGACGCCGCCGATAAACACA 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43
                                                     AACGCGTCCAAATACGCATTCGGGTTCAACCAGGTCAGCAGGTTGCCATTGCCATCAACATGGGC
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                                                                                           TITACCCAAACCCGCTGCTTATCGACGCTCACCTCCACCCGCACCCGGTTGCGGCGTGTCA
                                                                                                                 522 TITACCCAAACCCGCTGCTTATCGACGCTCACCTCCACCCGGACCCGGTTGCGGTGTGTCA
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                               AACGCGTCCAAATACGCATTCGGGTTCAACCAGGTCAGCACGATTGCCATCAACATGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glutamicum gene #23 encoding metabolic pathway protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 TAATATAGCTTCATGAACCCCATTCAACTGGACACTTTGCTC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-2000; 2000WO-IB002035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-2000; 2000US-0187970P.
23-JUN-2000; 2000US-00606740.
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Kim J, Lee H, Hwang B;
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CACCAGCGGGAACCAGATCAGGCTTGCCGCGAAACGCGCCAGCGGCGAAAATCCACCGTCC
                                                                                             CACCAGCGGGAAACCAGATCAGGCTTGCCGCGAACGCGCCAGCGGCGAAAAATCCACCGTCC
                                                                                                                                               GGTGTCGCCGTATTGCGCGCCGCCGCCGATAAACACAAAACGCGTCCAAATACGCATT
                                                                                                                                                                                      531 GGTGTCGCCGTATTGCGCGCCGGCGGCCGATAAACACAAAACGCGTCCAAATACGCATT
                                                                                                                                                                                                                               889 CGGGTTCAACCAGGTCAGCACGATTGCCATCAACATGGGCTTTACCCAAACCCGCTGCTT
                                                                                                                                                                                                                                                                                                                                       411 ATCGACGCTCACCTCCACCCGCACCCGGTTGCGCGTGTCAGTGGCCACCGCCGCAACCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1309 AAGACTGGCCCCCAAAAGCAGACCTGTAATGAAGATTTCCATGATCACCAT 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 AAGACTGGCCCCCAAAAGCAGACCTGTAATGAAGATTTCCATGATCACCAT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mizoguchi H, Ando S, Hayashi M, Ochiai K,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C glutamicum coding sequence fragment SEQ ID NO: 3455.
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07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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Tateishi N,
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AAH68420/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to DNA encoding variants of protein with loop region and six hydrophobic helixes which facilitates excretion of Lysine and/or L-arginine to outside of cell of a methanol assimilating bacterium when introduced into the bacterium. The method is used for encoding a protein which facilitates excretion of L-lysine, L-arginine or both of these L-amino acids to outside of a cell of a methanol assimilating bacterium when DNA of the method is introduced into the bacterium. The present sequence represents a lyse protein from Breviation and accepting sequence. (Updated on 27-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        708
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                                           Novel DNA encoding variant of LySE protein from a coryneform bacterium, when introduced into methanol assimilating bacterium, facilitates excretion of L-lysine and/or L-arginine to outside of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      649 CIAACCCATCAACATCAGTTTGATGGCCAATGCGGTCATCACAACTGCCACGACGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                   TAATATAGCTTCATGAACCCCATTCAACTGGACACTTTGCTC 1450
                                                                                                                                    42 TAATATAGCTTCATGAACCCCATTCAACTGGACACTTTGCTC 1
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Pred. No. 5.7e-211;
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/product= "lysE protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                         LysE protein encoding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                  L-lysine; L-arginine; LysE; ds.
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ID ACC80941 standard; DNA; 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum.
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(first entry)
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11-AUG-2003
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950 TCGACGCTCACCTCCACCCGCACCCGGTTGCGCGTGTCAGTGGCCACCGCCGAACCGCCC 1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a gene from a high temperature-resistant coryndeform microbe that encodes a heat-resistant lyain biosynthetic enzyme. The enzyme has aspartate-semialdehyde dehydrogenase activity can be used for growing amino acid-producing microbes. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A heat-resistant lysin biosynthetic system enzyme gene of a high temperature-resistant coryneform microbe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 698.6; DB 4; Length 1568;
Pred. No. 7e-207;
0; Mismatches 454; Indels 16;
1312 ACTGGCCCCCAAAAGCAGACCTGTAATGAAGATTTCCATGATCACCAT 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1568 BP; 258 A; 525 C; 490 G; 295 T; 0 U; 0 Other;
                       48 ACTGGCCCCCAAAAGCAGACTGTAATGAAGATTTCCATGATCACCT
                                                                                                                                                                                                                                                                                                                                         Heat-resistant, lysin biosynthesis, enzyme; coryneform; aspartate-semialdehyde dehydrogenase; lysE; ds.
                                                                                                                                                                                                                                                                                            enzyme lysE DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence encodes an enzyme of the invention
                                                                                                                                                                                                                                                                                              C. thermoaminogenes lysin biosynthetic
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                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium thermoaminogenes
                                                                                                            RESULT 11
AAH45375/c
ID AAH45375 standard; DNA; 1568 BP.
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                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 68.4
Matches 1017; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AJIN ) AJINOMOTO KK.
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No. 7.9e-210; Indels
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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Pred. No. 9.5e-185;
                                              Claim 1; SEQ ID NO 3454; 246pp + Sequence Listing; English
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Matches 627; Conservative
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   CACCAGGGGAACCAGATCAGGCTTGCCGCGAACGCGCCAGCGGCGAAAATCCACCGTCC 533
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                                 GGTGTCGCCGTATTGCGCCGCCGACGCCGCCGATAAACACAAAACGCGTCCAAATACGCATT
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                                                                                                               CGGGTTCAACCAGGTCAGCACGATTGCCATCAACATGGGGCTTCACCCCAAACCCGCTGCTT
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                                                             GGTGTCGCCGTATTGCGCCGCCGACGCCGATAAACACACAAAACGCGTCCAAATACGCATT
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                                                                                                                                                                                                                                                  CCAAAGGCGTGTCATCGGCACGGTTGGTTTCTTTCTTCATGATCTGTGGCGCTTCCA
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Ozaki A;
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Ikeda M,
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Senoh A,
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03-AUG-2000;
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identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.

AAF68082 and AAF68082 represent sequencing primers which are used in an
                                                                                                                                                                                                                                                                         1 AGATACTCCTTTGGAAGAAACCATGTACGCATTGCGTGACATTGTTGCGTCTGGAAAGGC
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                                                                                                                                                                                              Length 993;
                                                                                                                                                         Sequence 993 BP; 222 A; 247 C; 277 G; 247 T; 0 U; 0 Other;
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Pred. No. 2.7e-140;
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                                                                                                                   example from the present invention
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                                                                                                                                                                                              tch 20.4%; al Similarity 99.0%; 499; Conservative
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Best Local Similarity
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                                                                                                             Corynebacterium glutamicum; brevibacterium lactofermentum; MCT; membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation; genome mapping; genetic engineering; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacteium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for
                                                                          Corynebacterium glutamicum MCT protein encoding DNA SEQ ID NO:669
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P-PSDB; AAB76844.
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AAF68077;
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The invention relates to an isolated nucleic acid comprising any one of the fell antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense of acid; (2) a host cell containing the vector; (3) an isolated polypeptide acid; (4) an antibody capable of specifically binding onlypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound,'s activity; (11) a culture comprising strains in which the gene or organism acts; (9) manufacturing an antibiotic; (10) profilling to organism acts; (9) manufacturing an antibiotic; (10) profilling the compound's activity; (11) a culture comprising strains in which the capen or product a organism acts; (12) determining the extent compound that inhibits are useful for proliferation of an organism; or (13) identifying the target of a compound that inhibits the proliferation of an organism; or class or a collection of a proliferation or an enroles or a gene and are useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aurens, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; SEQ ID NO 17521; 1766pp; English
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Carr GJ,
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                   (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                      Zamudio C,
Trawick JD,
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Wall D,
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Sequence 1095 BP; 264 A; 247 C; 311 G; 273 T; 0 U; 0 Other; electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Gaps ö 12.9%; Score 305.8; DB 7; Length 1095; 67.1%; Pred. No. 3.5e-84; tive 0; Mismatches 212; Indels 0; 433; Conservative Query Match Best Local Similarity Matches 433; Conservat

121 GGCGGAGGAGGCTGCCGCTTCTGATTCATCAGCCAAGCTATTCCATCATTAATCGTTG 180 9 AGATACGCCTTTGGAAGAAACTGCATATGCTTTGCGAGACATCGTGGCATCCGGCAAGGC rescrargrescarrirecrecraresacersaacraacesesasarrer GGTGGAGGAACCGGGCGATGACGGTGAGAACTTGTTGCAGTCAGCTGCCAACAATGGTCT 1 AGATACTCCTTTGGAAGAAACCATGTACGCATTGCGTGACATTGTTGCGTCTGGAAAGGC 450 61 510 181 q ð g g ₽ à

990 TAATAATCITIGAGITICAGCGITIGAGGAACGCAATTATAITIGACACTGITIGCCAAGGACGC 1049 480 GAACAATATTGATATGGTCCGCAAGCTCAATGACATCGCCCAGGAACGCGGGCAGTCACT 420 810 TAAAAATCTIGACATGGGGGGGGAATGATTTAGGGTTACGACGTGGCCAAACGTT 869 481 GACCAGIGCAITIGAITIGGIGCITICGICAGITIGAGCAGCIGGACAACAGCCITIGAITICACI 540 989 541 CAACAACTIGGAGIITITCIGACGCCGAGIIGGAGGCGAICGAIGAGAIITCCCACGACGC 600 750 cereccaeresarreacesecaecaecaecaesaerecrresecaaagarecreaace 809 241 TGGCGTCATTGCTTTCTCACCACTTGCGCAGGCCTGCTCACGGACAAATATCTCGATGG 300 690 GGGTGTTATTGCATTTTCGCCACTTGCACAGGGCTTTTAACTGACAGGTATCTCGAGGG 301 AATTCCAGAGGGTTCCCGCGCCAGCCAGGGTAAGTCCCTGTCTGAGGGCATGTTGAACGT TGCGCAGATGCCGCTTGCATGGGTGCTGCGCGAGCAAGGAGAGTACGGCGCGCGATACCGT 930 AACCAGTGCGTTGATCGGAGCATCGTCGGTAGCGCAGTTGGATCAAAATCTGGGAGCTCT .050 recaarraararrirececeerecracrecrecaeerreace 1094 601 CGGCATCAACATTTGGGCGAAGGCCACCGATTCCAAAACCCGCGA 421 셤 à 셤 8 셤 ò 셤 Š à 음 ਨੇ

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Search completed: March 15, 2004, 14:59:19 Job time : 971.046 secs

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RESULT 1
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4735, Ap
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7908, Ap
7643, Ap
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4674, Ap
1694, Ap
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5488, Ap
7723, Ap
22, Appl
                                                                                       March 15, 2004, 13:47:35 ; Search time 178.837 Seconds (without alignments) 7366.769 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-103-840A-2
US-08-103-840A-2
US-08-20-812-20
US-08-921-177-20
US-08-36-577C-20
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US-09-25-991A-7571
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US-09-252-991A-7723
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O	28	43	1.8		4	US-09-543-681A-800	Sequence 80	800, App
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	30	42	1.8		4	US-09-252-991A-16286	Sequence 16	16286, A
O	31	42	1.8		4	US-09-252-991A-15990	Sequence 15	.5990, A
	32	42	1.8		4	US-09-252-991A-16513	Sequence 16	16513, A
	33	41.6	1.8		4	US-09-621-976-15639	Sequence 15	15639, A
	34	40.6	1.7	696	4	US-09-252-991A-345	Sequence 34	345, App
U	35	40.4	1.7		4	US-09-252-991A-5423	Sequence 54	5423, Ap
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	38	39.6	1.7	_	~	US-08-492-027A-9	Sequence 9, Appli	Appli
υ	39	39.4	1.7	505	4	US-09-621-976-15639	Seguence 15	.5639, A
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	45	37.6	1.6	4411529	m	US-09-103-840A-1	Sequence 1	l, Appli

ALIGNMENTS

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Sequence 17, Application US/08390878
Patent No. 5700633
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us-09-105-117k-3.rni

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Pred. No. 5.9e-26;
0; Mismatches 423;
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                                                                                                          4.0
PRIOR APPLICATION NUMBER: 60/097,936
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: FastSEQ for Windows Version SEQ ID NO 12
LENGTH: 909
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US-09-894-844-12
                                                                                                                                                                                                                                                                                                                                                    Query Match 5.1%;
Best Local Similarity 49.5%;
Matches 433; Conservative
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APPLICANT: Behr, Marcel
APPLICANT: Small, Peter
APPLICANT: Schoolnik, Gary
APPLICANT: Wison, Michael A.
TITLE OF INVENTION: Molecular Differences Between Species of
TITLE OF INVENTION: the M. Tuberculosis Complex
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CURRENT APPLICATION NUMBER: US/09/894,844
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: 09/318,191
PRIOR FILING DATE: 1999-05-25
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APPLICANT: WHITE, Own R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
UNMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO: 1
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Pred. No. 9.8e-24;
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) ORGANIGN: Mycobacterium tuberculosis

) OTHER INFORMATION: H37Rv

US-09-103-640A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09103840A; Patent No. 629432B; GENERAL INFORMATION: APPLICANT: FLEISCHWAN, Robert D. APPLICANT: FLEISCHWAN, Robert D.
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Matches 433; Conservative
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Pred. No. 9.8e-24;
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CURRENT APPLICATION NUBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                       APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VBNTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                  Sequence 2, Application US/09103840A
Batent No. 6294338
GENERAL INFORMATION:
APPLICANT: PLEISCHMAN, Robert D.
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                                                                                                                                                                                                                                                                                                   Length 5541;
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                                                                                                                                                                                                                                                                                                     4.2%; Score 100.8; DB 1; 50.5%; Pred. No. 2.2e-19;
                                                                                                                                                                                                                                                                                                                             Pred. No. 2.2e-19;
0; Mismatches 332;
                                                                                                                                                                                                  ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-625
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; Sequence 20, Application US/08920827
; Patent No. 5770375
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INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 5541 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                     Genomic DNA
                                                                                                                                                                                                                                                                                                                                                       Matches 386; Conservative
                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                             ORIGINAL SOURCE:
                                                                            TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                     MOLECULE TYPE:
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     INFORMATION
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                                                                                                        2229462 ACCGAGCGGAACCCGGTGCCGGGCTGCCGGGTGCACCCGCTGGGTGAAATGCGCTACCTA 2229403
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       2229522 GAGGACCAGGACCATTCCGCGCGGCTGCTACGGGAGGGTGTGGCGATGGGCGCGCGGTGACC 2229463
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                                                                                                                                                                                                                                                         1967 GCGATGCCCGTCTTACGCTTCGGTCCCAAAGATGTGCTTCAAGACCGTGACCTGGACGGG 2026
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                                                         1847 CGTGAAGCTAATCCCGTGGCGGATGTGAAGTAGTAGAACTTGGAACCATGCGCCCACTTG 1906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2144 CCCATGCTAAAAGCAGGAGAAGTGATCCTCCTCGATGAGATACCCATTGACACCCACACGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08920812
Patent No. 5763188
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Watsuhisa, Akio
APPLICANT: Watsuhisa, Akio
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SECHENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
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REGISTATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPONS: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
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APPLICATION NUMBER: US/08/920,812
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/362,577
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TTORNEY/AGENT INFORMATION:
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US-08-920-812-20/c
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2966 ----TGATCGCGTGACGTCGGTATTGATTGGTGC-CAGCCGCGCGGACATAGTTGAGGAA 2911
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                                                                                                          409 CGGGCAGTCACTTGCGCAGATGGCGCTTGCATGGGTGCTGCGGCGAGCAAGGAGAGTACGG 468
                                                                                                                                                                                                             469 CGCGGATACCGTGACCAGTGCATTGATTGGTGCTTCGTCAGTTGAGCAGCTGGACAACAG 528
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                                                                                                                                                     3011 TGGACAATCAATGGCGAAATGGCGTTAAGCTGGTTGCTGAAAGA-------
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GENERAL INFORMATION:
APPLICANT: Matsuhisa, Akio
APPLICANT: Ushara, Hirotsugu
APPLICANT: Ushara, Hirotsugu
APPLICANT: Ushara, Hirotsugu
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease; CORRESPONDENCE: 25
CORRESPONDENCE: 25
CORRESPONDENCE: 25
CORRESPONDENCE: 300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe for Diagnosing Infectious Disease
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COUNTRY: United States of America
ZIP: 6666-640.

ZIP: 6666-640.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

PPLICATION NOBER: U9/08/921,177

FLING DATE: 29-AUG-1997

CLASSIFICATION: 435

PRIOR APPLICATION NOBER: US 08/362,577

FILING DATE: 27-MAR-1995

ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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STREET: 65...
TTW: Chicago
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                                                                                                     Probe for Diagnosing Infectious Disease
                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-AUG-1997
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Pred. No. 2.2e-19;
0; Mismatches 332;
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                                                                                                                                                                                                                                                          STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
                                                                                                                                                                                                                                                                                                                             COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Clinical Isolate EC-625
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ATTORNEY/AGENT INFORMATION:
NAME: Rin-Lautes, Li-Heien
REGISTRATION NUMBER: 33,547
REFERRNCE/DOCKET NUMBER: 1903
TELECOMMUNICATION INFORMATION:
APPLICANT: Ohno, Teuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Ushara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for i
NUMBER OF SEQUENCES: 25
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INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.5%;
Matches 386; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
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312/474-0448
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MOLECULE TYPE:
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US-08-920-827-20
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Š 셤 ₹ ద δ g à a õ d ò Probe for Diagnosing Infectious Disease

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TITLE OF INVENTION:
NUMBER OF SEQUENCES
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                                                                                                                                  Query Match 4.2%; Score 100.8; DB 1; Best Local Similarity 50.5%; Pred. No. 2.2e-19; Matches 386; Conservative 0; Mismatches 332;
                                                                       Clinical Isolate EC-625
                                                         Escherichia coli
                  MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGGATAAAAGCGG
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  linear
                                                             ORGANISM:
                                                                           ; STRAIN: CUS-08-921-177-20
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US-08-362-577C-20/c
; Sequence 20, Application US/08362577C
; Patent No. 5807673
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Warsuhisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji

Ohno, Tsuneya Matsuhisa, Akio Uehara, Hirotsugu Eda, Soji

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                                                                                                                                                   COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,577C
FILING DATE: 27-MAR.1995
CLASSIFICATION: 536
                     2: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 4.2%; Score 100.8; DB 1;
Local Similarity 50.5%; Pred. No. 2.2e-19;
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0; Mismatches 332;
                                                                                                                                                                                                                                                                                                                                                                                      NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REPERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPRAX: 312/474-0448
                                                                                 STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Bacherichia coli
; STRAIN: Clinical Isolate BC-625
US-08-362-577C-20
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 5541 base pairs
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CORRESPONDENCE ADDRESS:
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Sequence 5370, Application US/09489039A

Sequence 5370, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICATION SEPECTOR Et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR PALICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 1095

TYPE: DNA
                                                                                                                 3416 AAATACGCCGATGGAAGAAGAACCGCCTCTGCGCTCATGCGGTACAAGCGGTAAGGC 3357
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                                                                                                                                                                                                                       3296 GCGCGAGTGGAAAATTCCGCTGTTAATTCATCAACCTTCGTACAATTTACTGAACCGCTG 3237
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                                                                         1 AGATACTCCTTTGGAAGAAACCATGTACGCATTGCGTGACATTGTTGCGTCTGGAAAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469 CGCGGATACCGTGACCAGTGCATTGATTGGTGCTTCGTCAGTTGAGCAGCTGGACAACAG
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                          Gaps
                               46;
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  Pred. No. 2.2e-19;
0; Mismatches 332; Indels
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     50.5%;
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Best Local Similarity 50.5
Matches 386; Conservative
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COUNTRY: United States of America
ZIP: 6060-6402
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRINI APPLICATION NATE: US/08/920,828
FILING DATE: 29-AUG-1997
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TELECOMNUNICATION INPORMATION:
TELEPHONE: 312/474-6300
TELEPAX: 312/474-0448
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT: INFORMATION:
NAME: Rin-Laures, Li-Heien
REGISTRATION NUMBER: 33,547
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STRAIN: Clinical Isolate BC-625
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Patent No. 5853998
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APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for I
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SEQUENCE CHARACTERISTICS:
LENGTH: 5541 base pairs
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nucleic acid
EDNESS: double
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APPLICANT: Ohno, 1
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STREET: 0...
Tmv: Chicago
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us-09-105-117k-3.rni

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Sequence 791, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GAYT BRETON:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRAE

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REPERBNCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09
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SEQ ID NO 791
LENGTH: 936
TYPE: DNA
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US-09-543-681A-791
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AMOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR PELICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
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Pred. No. 5.2e-14;
0; Mismatches 216; Indels
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Pred. No. 1.1e-13;
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Patent No. 6610836
GENERAL INFORMATION:
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           , ORGANISM: Klebsiella pneumoniae US-09-489-039A-5370
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Best Local Similarity 51.5%;
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SEQ ID NO 4735
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US-09-489-039A-4735
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      PRIOR APPLICATION NUMBER: US (PALOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 7644 LENGTH: 900
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGGCGCGTATCCATTGTCCCGTCGCCGAAGGTTTTGGTGAGGCAATTCGCCGAGGCC 2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2109 TTGGTTGGGGACTTCTTCCCGAAACCCAAGCTGCTCCCATGCTAAAAGCAGGAGAAGTGA 2168
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                                                                                                                                                                                                                                                                                                                           0; Mismatches 391;
                                                                                                                                                                                                  Score 73.4; DB 4
Pred. No. 1.2e-11
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Patent No. 6551795
                                                                                                                                                                                            Query Match 3.1%;
Best Local Similarity 44.9%;
Matches 324; Conservative
ORGANISM: Proteus mirabilis
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US-09-252-991A-7644
                    ; ORGANISM: Fron
US-09-543-681A-791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          626 CGTCCGG-------CTTGATCGATGCATTAAAAGCTGATGGTGCCGGGTTGA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGCTTTCTCACCACTTGCGCAGGGCCTGCTCACGGACAAATATCTCGATGGAATTCCAG 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        731 ATACTITICAAAATCCATCCAACCAACAAGGCCACTITIGCTAAGGGCAAAGAGGCTGTGG 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  791 TTAAGCAACTAAATGCGCTTAATGAAATTGCGCATGATCGTGACCAAACCCTGAGTCAAA 850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     893 TGATCATTGGGACGACCTCAGTTGAACACCTTCAGGATAACCTTAAAGGAACGGAACATC 952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 AACCGGGCGATGACGGTGAGAACTTGTTGCAGTCAGCTGCCAACAATGGTCTTGGCGTCA
                                    Sequence 24, Application US/09724623

Patent No. 6476209

GENERAL INFORMATION:

APPLICANT: Glenn, Matthew

APPLICANT: Lubbers, Mark W

APPLICANT: Lubbers, Mark W

TITLE OF INVENTION: Polynucleotides, materials incorporating

TITLE OF INVENTION: them, and methods for using them.

FILE REFERENCE: 1048U1

CURRENT PILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 124

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.7%; Score 64; DB 4; Length 100:
47.9%; Pred. No. 7.8e-09;
tive 0; Mismatches 270; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     549 TGGAGTTTTCTGACGCCGAGTTGGAGGCGATCGATGAGATTT 590
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Lactobacillus rhamnosus
US-09-724-623-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 47.9
Matches 279; Conservative
RESULT 14
US-09-724-623-24
                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 24
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US-09-252-991A-7908/C
; Sequence 7908, Application US/09252991A
; Patent No. 6551795
; PERERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        710 ATCCAGGGCCACACCTTGGGGGCTGGACAGGGGGGTGACAATGCTGCTGCTGCGGCGGAAACCC 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  638 Accadedecadestracecededecececadecadededecateceatecedededededeses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           698 TATCCCCGGAACAGCAGTTGCGCGGCCATGCCCAGCATCATGGCCGCCACCATCAGGTCG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       770 ACCAGCGGGAACCAGATCAGGCTTGCCGCGAACGCGCCAGCGGCGAAAATCCACCGTCCG 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      830 GIGICGCCGIAITGCGCCCCCCCCCCCCCGAIAAACACACAAAACGCCTCCAAATACGCAITC 889
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                                                                                                                                                                                                                                                                                                                                                                                      Length 699;
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54.6%; Pred. No. 2.9e-08;
ive 0; Mismatches 117; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 egeringageageereacceccaerececa 434
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTIC;
FILE REPERRENCE: 10/196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-7
; NUMBER OF SEQ ID NOS: 33142
; NUMBER OF SEQ ID NOS: 33142
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Job time : 197.837 Becs
                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                      148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Best Local S:
Matches 148
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March 17, 2004, 00:51:03; Search time 851.071 Seconds (without alignments) 10269.549 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/PCT_NBW_PUB_seq:*

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10: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

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13: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

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15: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2432557 seqs, 1840798884 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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2374
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

						SUMMARIES	
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Result	بد		Query				
No.		Score	Match	Match Length DB	四	£	Description
υ	н	2374	100.0	2374 14	14	US-10-196-232-24	Sequence 24, Appl
	21	2374	100.0	100.0 3309400	σ	US-09-738-626-1	Sequence 1, Appli
	ж	993	41.8	993	10	US-09-746-660A-47	Sequence 47, Appl
	4	870	36.6	870	σ	US-09-738-626-3456	Sequence 3456, Ap
U	Ŋ	822	34.6	822	70	US-09-746-660A-51	Sequence 51, Appl
ט	و	711	29.9	711	14	US-10-166-142-7	Sequence 7, Appli
U	7	708	29.8	708	σ	US-09-738-626-3455	Sequence 3455, Ap
υ	80	8.969	29.4	712	14	US-10-166-142-9	Sequence 9, Appli
	6	627	26.4	627	9	US-09-738-626-3454	Sequence 3454, Ap
7	9	485.2	20.4	993	12	US-10-627-476-669	Sequence 669, App
-	⇉	305.8	12.9	1095	12	US-10-282-122A-17521	Sequence 17521, A
_	7	302.8	12.8	879	12	US-10-282-122A-17523	Sequence 17523, A
	9	164.4	6.9	1026	15	US-10-369-493-35374	Sequence 35374, A
-	4	164.4	6.9	1026	15	US-10-369-493-38826	Sequence 38826, A
-	2	164.4	6.9	1028	15	US-10-369-493-38124	Sequence 38124, A

Seguence 13437, A	Sequence 14749, A	Sequence 26429, A	Sequence 12, Appl	Sequence 12, Appl	Sequence 28444, A	Sequence 1110, Ap	Sequence 1, Appli	Sequence 11887, A	Sequence 1151, Ap	Sequence 1, Appli	Sequence 14390, A	Sequence 37651, A	Sequence 19965, A	Sequence 7020, Ap	Sequence 38764, A	Sequence 39389, A	Sequence 33379, A	Sequence 77, Appl	Sequence 1450, Ap	Sequence 6195, Ap	Sequence 20492, A	Sequence 12754, A	Sequence 41572, A	Sequence 23370, A	Sequence 1395, Ap	Sequence 41645, A	Sequence 9644, Ap	Sequence 40108, A	Sequence 38717, A
US-10-282-122A-13437	US-10-282-122A-14749	US-10-282-122A-26429	US-09-894-844-12	US-10-388-902-12	US-10-282-122A-28444		US-10-156-761-1	US-10-282-122A-11887		US-10-156-761-1	US-10-282-122A-14390	US-10-369-493-37651	US-10-282-122A-19965	US-10-282-122A-7020	US-10-282-122A-38764	US-10-282-122A-39389	US-10-282-122A-33379	US-09-974-300-77	US-10-260-238-1450	US-09-815-242-6195	US-10-282-122A-20492	US-10-282-122A-12754	US-10-282-122A-41572	US-10-282-122A-23370	US-09-738-626-1395	US-10-282-122A-41645	US-09-815-242-9644	US-10-282-122A-40108	US-10-282-122A-38717
12	12	12	6	15	12	14	14	12	14	14	12	15	12	12	17	12	12	6	12	σ	12	12	12	12	σ	12	6	12	12
1041	897	606	606	606	912	954	9025608	1041	993	9025608	1107	1026	1038	1041	666	666	1035	988	745	894	894	666	606	990	1077	990	894	894	894
5.6	5.2	5.2	5.1	5.1	5.1	5.1	5.1	4.9	4.9	4.9	4.8	4.6	4.6	4.5	4.4	4.4	4.1	3.9	3.6	3.5	3.5	3.4	3.4	3.3	3.3	3.3	3.5	3.5	3.2
132.6	123.8	122.8	121.2	121.2	121.2	120.8	120.8	116.4	115.2	115.2	114.8	108.6	108.6	107	105.2	105.2	97.4	93.2	86.4	82.6	82.6	81.4	79.8	78.2	78	77.4	76.2	76.2	75.2
16	17	18	19	20	21	22	23	24	25	c 26	27	28	29	30	31	32	33	34	35	36	37	38.	39	40	c 41	42	43	44	45

ALIGNMENTS

2374 AGATACTCCTTTGGAAGAAACCATGTGCGTGACGATGCGTGACATTGTTGTTGCGTCTGGAAAGGC 2315 61 TCTTTACGTGGGTATTTCTTCCTACGGTCCAGAGCTCACAGCGGAGGCGGCTGAGTTCAT 120 1 AGATACTCCTTTGGAAGAAACCATGTACGCATTGCGTGACATTGTTGCGTCTGGAAAGGC 60 Ouery Match 100.0%; Score 2374; DB 14; Length 2374; Best Local Similarity 100.0%; Pred. No. 0; Matches 2374; Conservative 0; Mismatches 0; Indels 0; APPLICANT: YAMAGUCHI, MIKIKO
APPLICANT: YAMAGUCHI, MIKIKO
APPLICANT: TTO, HISAO
APPLICANT: YASUEDA, HISASHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-ARGININE
FILE REFERENCE: 225391US0
CURRENT APPLICATION NUMBER: US/10/196,232
CURRENT APPLICATION NUMBER: US/10/196,232
FRIOR PILING DATE: 2002-07-17
PRIOR PILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.1 TYPE: DNA ORGANISM: Corynebacterium glutamicum Sequence 24, Application US/10196232; Publication No. US20030113899A1; GENERAL INFORMATION: NAME/KEY: CDS ; LOCATION: (1025)..(1723) ; OTHER INFORMATION: US-10-196-232-24 JS-10-196-232-24/c SEQ ID NO 24 LENGTH: 2374 FEATURE: ਨੇ 음 ð 셤

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Gaps

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1561 GGTATCGCGCACCCAACCGGCCAAAGCAACCGAAGCGGGTGAAGTCCTTGTGCAAGCAGC 1620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAACGAGGTAGCTTCTTGGGGTGGAGCAACGCTCACGCTGCGCTTGGAAGATGAAGCGCA 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTITIECT CTATCATIGATGAAGGCAGCTTCGAAGGCGCCTCCTTAGCCCTTTCCAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 AATCCGTTAACCATCGCCATCAACGCAGATTCGCTATCCACATGGTTTCCTCCCGTGTT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 CAACGAGGTAGCTTCTTGGGGTGGAGCAACGCTCACGCTGCGCTTGGAAGATGAAGCGCA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: RXA01393
US-09-746-660A-47
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; Sequence 47, Application US/09746660A
; Publication No. US20030049804A1
; GENERAL INFORMATION:
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APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
APPLICANT: Haberhauer, Gregor
APPLICANT: Liee, Heung-Schick
APPLICANT: Hanng, Byung-Joon
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APPLICANT: Hwang, Byung-Joon
TITLE OF INVENTION: CORYNBARCTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: MSTABOLIC PATHWAY PROTEINS
FILE REPERENCE: BGI-121CP2
CURRENT APPLICATION NUMBER: US/09/746,660A
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Publication No. U820030049804A1
GENERAL INFORMATION:
APPLICANT: Fompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Alberhauer, Gregor
APPLICANT: Haberhauer, Gregor
APPLICANT: Kim, Unn-Won
APPLICANT: Lee, Heung-Schick
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                                                                                     CTCATTGCGGGATGCCTACATGGTTGATGGGAAACTAGATTGGGCTGCGGTGCCGTCTT
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APPLICANT: NAKGAMA, SETOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TEELBH, MASATO
APPLICANT: TEELBH, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERBREE: 249-125
CURRENT FILING DATE: 2000-12-18
FRICH PRICHATION NUMBER: UP 99/377484
FRICH PLING DATE: 1999-12-16
FRICH PLING DATE: 2000-04-07
FRICH PLING DATE: 2000-04-07
FRICH PLING DATE: 2000-06-03
FRICH FILING DATE: 2000-06-03
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Publication No. US20020197605A1
GENERAL INFORMATION:
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US-09-738-626-3456
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Matches 870
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WS-10-166-142-7/c

| Sequence 7, Application US/10166142
| Sequence 7, Application WS/10166142
| GENERAL INFORMATION |
| APPLICANT GINAI, YOSHIVA |
| APPLICANT GINAI, YOSHIVA |
| APPLICANT THORMATION |
| APPLICANT SASUEDA, HISASH|
| TITLE OF INVERTION WETHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL |
| TITLE OF INVERTION WINDHER: US/10/166,142 |
| CURRENT FILING DATE: 2002-06-11 |
| PRIOR APPLICATION NUMBER: JP 2001-1777075 |
| PRIOR APPLICATION NUMBER: JP 2001-1777075 |
| NUMBER OF SEQ ID NOS: 10 |
| SEQ ID NO 7 |
| LENGTH: 211
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                                                                                                                                                     349 ATGATCACCATCGTGACCTATGGAAGTACTTAAGTAAATGATTGGTTCTTAACATGGTT 1408
                                                     1289 TGCGGTCCGATGGACAGTAAAAGACTGGCCCCCAAAAGCAGACCTGTAATGAAGATTTCC 1348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           709 GATCCAGCGCCACACCTTGGGGCTGGACAGCGGGCGTGACAATGCTGCTGCCGCAAACC 768
  222 ACGAGAAGCAACGCAATGAGTCCTTCGCGCTTAATTCCTTGTTTAATCACCAGTACATTC 163
                                                                                                                                                                                     102 ATGATCACCATCGTGACCTATGGAAGTACTTAAGTAAAATGATTGGTTCTTAACATGGTT 43
                                                                                  829 GGTGTCGCCGTATTGCGCGCCGACGCCGCTAAACACAAAGGCGTCCAAATACGCATT
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CTHER INFORMATION:
US-10-166-142-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 402 Argancrigrosciectriceaectristristearosciectriresciecearoscoanaec 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                869 AACGCGTCCAAATACGCATTCGGGTTCAACCAGGTCAGCACGATTGCCATCAACATGGGC 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           749 AATGCTGCTGCGCCGAAACCCACCAGCGGGAACCAGATCAGGCTTGCCGCGAACGCGCCA 808
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PRICAR PULLING DATE: 2000-12-22
PRICAR PULLCATION NUMBER: 09/606740
PRICAR PULLING DATE: 2000-06-23
PRICAR APPLICATION NUMBER: 09/603124
PRICAR FILING DATE: 2000-06-23
PRICAR APPLICATION NUMBER: 60/141031
PRICAR APPLICATION NUMBER: 60/142101
PRICAR APPLICATION NUMBER: 60/142101
PRICAR APPLICATION NUMBER: 60/148613
PRICAR APPLICATION NUMBER: 60/18970
PRICAR APPLICATION NUMBER: 60/18970
PRICAR APPLICATION NUMBER: 60/18970
PRICAR APPLICATION NUMBER: 60/18970
PRICAR APPLICATION NUMBER: 1999-00-03-09
PRICAR APPLICATION NUMBER: DE 19931420.9
PRICAR APPLICATION NUMBER: 19931420.9
PRICAR APPLICATION NUMBER: 19931420.9
NUMBER OF SED ID NOS: 125
SOFTWARE: PATENTIN VERS: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
OCYMPANEM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (101) .. (799)
; OTHER INFORMATION: RXA01394
US-09-746-660A-51
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Matches 822; Conservative
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LENGTH: 822
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Sequence 9, Application US/10166142

Publication No. US20030124687A1

GENERAL INPORMATION:

APPLICANT: GINAI, YOSHIYA

APPLICANT: TASUEDA, HISASHI

TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL

TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL

TITLE OF INVENTION: ASSIMILATING BACTERIUM

FILE REFERENCE: 223789US

CURRENT APPLICATION NUMBER: US/10/166,142

CURRENT FILING DATE: 2002-06-11

FRIOR APPLICATION NUMBER: JP 2001-1777075

FRIOR FILING DATE: 2001-06-12

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Version 3.1

SSEC ID NO 9
                                                                                                                                                                                           952 GACGCTCACCTCCACCCGCACCCGGTTGCGCGTGTCAGTGGCCACCGCCGAACCGCCCAA 1011
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APPLICANT: MAZOCHAL, MIKURO
APPLICANT: OCHIAL, KEIKO
APPLICANT: OCHIAL, KEIKO
APPLICANT: YOKOI, HAKUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKTHIRO
APPLICANT: SENOH, AKTHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
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Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: MAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIDOSUSHION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SE
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APPLICANT: Roger, Burkhard
APPLICANT: Schoder, Hartwig
APPLICANT: Schoder, Hartwig
APPLICANT: Caldar, Oskar
APPLICANT: ABDERLAUER, Gregor
TITLE OF INVENTION: INVOLVENDEN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: INVOLVENDENT TRANSPORT
TITLE OF INVENTION: INVOLVENDENT MARKANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: INVOLVENDENT MARKANE
TITLE OF INVENTION: INVOLVENTON
TITLE OF INVENTION: UNMERR: 03/10/627,476
CURRENT RPLING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: 03/602,787
PRIOR APPLICATION NUMBER: 03/602,787
PRIOR APPLICATION NUMBER: DE 1999-10/25
PRIOR PILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
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                                                                Gaps
                                                                ;
      Length 627;
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Query Match 26.4%; Score 627; DB 9; Lk Best Local Similarity 100.0%; Pred. No. 1.3e-198; Matches 627; Conservative 0; Mismatches 0;
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                                                                                              GGTGTCGCCGTATTGCGCCCCCGCCGCCGATAAACACACAAACGCGTCCAAATACGCATT 888
112 Greenregegernaarrechternaareaceagracarregegeregargeacagea 53
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APPLICANT: INEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPRENCE: 249-125
CURRENT FILING DATE: 2000-12-18
FRICA APPLICATION NUMBER: UP 90/73484
PRIOR PILING DATE: 1999-12-16
FRICA FILING DATE: 2000-04-07
FRICA FLIXED DATE: 2000-04-07
FRICA FLIXED DATE: 2000-04-07
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Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
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CURRENT PILLIGO NUMBER: US/10/282,122A

CURRENT TAPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

FRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-26

FRIOR PELICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

FRIOR APPLICATION NUMBER: 60/207,335

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/293,625

PRIOR APPLICATION NUMBER: 60/293,625

PRIOR APPLICATION NUMBER: 60/293,625

PRIOR APPLICATION NUMBER: 60/263,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/267,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR PRIOR FILING DATE: 2001-02-09

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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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Yamamoto, Robert
Forsyth, R.
                                           Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
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             FRIOR FILING DATE: 1999-07-08
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Pred. No. 5.8e-151;
0; Mismatches 3;
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; Sequence 17521, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
DE 19931563.9
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ORGANISM: Corynebacterium glutamicum
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.4%;
Best Local Similarity 99.0%;
Matches 499; Conservative
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OTHER INFORMATION: RXN03164
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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                                                                                                                                                                                990 TANTANTCITGAGITCAGCGTTGAGGAACGCAATTATAITGACACTGTTGCCAAGGACGC 1049
                           870 GGCACAGCTGGCTATTGCGTGGGGGCTGCGGGGAACAAGGCGATTATGGGGCCACAACGGT 929
                                                                                                      930 AACCAGTGCGTTGATCGGAGCATCGTCGGTAGCGCAGTTGGATCAAAATCTGGGAGCTCT 989
                                                                                                                                             541 CAACAACTIGGAGIIIIICIGACGCCGAGIIGGAGGCGAICGAIGAGAIITICCCACGACGC 600
TGCGCAGATGGCGCTTGCATGGGTGCTGCGCGAGCAAGGAGAGTACGGCGCGGATACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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NUMBER OF SEQ ID NOS: 78614
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Pred. No. 7e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                  Sequence 17523, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2003-02-05 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR PILING DATE: 2000-03-22 PRIOR PILING DATE: 2000-03-21 PRIOR PILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-23 PRIOR PILING DATE: 2000-05-26 PRIOR PILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR PILING DATE: 2000-09-06 PRIOR PILING DATE: 2000-09-06 PRIOR PILING DATE: 2000-09-09 PRIOR PILING DATE: 2000-09-09 PRIOR PILING DATE: 2000-10-23 PRIOR PILING DATE: 2000-11-27 PRIOR PILING DATE: 2000-11-27 PRIOR PILING DATE: 2000-12-22 PRIOR PILING DATE: 2000-12-22 PRIOR PILING DATE: 2000-12-22 PRIOR PILING DATE: 2000-12-22 PRIOR PILING DATE: 2001-02-03 PRIOR PILING DATE: 2000-12-22 PRIOR PILING DATE: 2000-12-22 PRIOR PILING DATE: 2000-12-22 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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59.2%;
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SEQ ID NO 17523
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-17523
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Sequence 35374, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Gladman, Barry S.
APPLICANT: Goldman, Barry S.
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
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Pred. No. 1.8e-43;
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     CURRENT APPLICATION NUMBER: US/10/369,493
                    CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3826
LENGTH: 1026
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US-10-369-493-38826
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianden, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B.
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Pred. No. 1.8e-43;
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 35374
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Publication No. US20030233675A1
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Matches 359; Conservative
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US-10-369-493-35374
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILLING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILLING DATE: 2002-02-1
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 38124
LENGTH: 1028
                                                                                                                                              TYPE: DNA ORGANISM: Agrobacterium tumefaciens
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657 bp mRNA linear EST 24-APR-2002
NF075E08IR1F1067 Irradiated Medicago truncatula cDNA clone
NF075E08IR 5', mRNA sequence.
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
Unpublished (2001)
Contact: May GD.
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Tel: 580 221 7391
Fax: 580 221 7391
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BQ155035.1 GI:20292094
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(bases 1 to 657)
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AL151258 Anopheles
                                               March 15, 2004, 13:43:00 ; Search time 6528.5 Seconds (without alignments) 10858.975 Million cell updates/sec
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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                   - nucleic search, using sw model
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/clone lib="MG1363 Random Sequence Tag Library"
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/note="vector: pSGWU2; Site 1: Smal; Library of
chromosomal fragments of L.lactis strain MG1363 was
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Suboltin,A., Enrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments (2002) In press
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cremoris genomic, genomic survey sequence.
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best homologue in strain IL1403 is nadR (98%)
Class: shotgun
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Pred. No. 9.5e-08;
                                                                                                                                                 Lactococcus lactis subsp. cremoris
Lactococcus lactis subsp. cremoris
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High quality sequence stop: 3207
Location/Qualifiers
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48.2%; Pred. No. 3.4e-11;
tive 0; Mismatches 255; Indels 0;
                                                                                                                                                                                         organism="Medicago truncatula"
    Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                   tissue type="seedlings"
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/db_xref="taxon:3880"
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CNS01MQH anopheles gambiae GSS T7 end of clone 22E24 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
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BP 191 91006 BVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - Web: www.genoscope.cns.fr)
2 (bases 1 to 830)
Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J. Direct Submission
Submitted (16-PEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.5%; Score 60.4; DB 29; Length 8 50.7%; Pred. No. 0.00013; Live 1; Mismatches 137; Indels
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                                             359 GGGTCAAAAATTGTATCAAATGGCGCTCGCCTCGGATGCTGCG 400
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         CGGGCAGTCACTTGCGCAGATGGCGCTTGCATGGGTGCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
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/# Btrain="PEST"
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/clone="22E24"
/clone_lib="NotreDame1"
/note="end : T7"
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Best Local Similarity 50.73
Matches 142; Conservative
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LOCUS
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TITLE
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JOURNAL
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CNS01MQH
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                                                                                                                                                                                                                                                                                                                   AF075981 GSS 29-AUG-2000 AF075981 Salmonella typhimurium LT2, Lambda DASH II Salmonella typhimurium genomic clone 390-T3, genomic survey sequence.
2051 AGCIGITACATCAGCTITGATIGGGGAAGTCGTCCGCAACAAATCATIGAAAATGTTGC 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 860)
Wong,R.M.-Y., Wong,K.K., Benson,N.R. and McClelland,M.
Sample sequencing of a Salmonella typhimurium LT2 lambda library:
comparison to the Escherichia coli K12 genome
FEMS Microbiol. Lett. 173 (2), 411-423 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella typhimurium
Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
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Pred. No. 9.9e-08;
0; Mismatches 160; Indels 22; Gaps
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/clone lib="Salmonella typhimurium LT2, Lambda
/note="Vector: Lambda DASH II; sequenced using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular Biology
Sidney Kimmel Cancer Center
31999 Science Park Road, San Diego, CA 92121, USA
Email: mcclelland@lifeci.sdsu.edu
                                                                                                                                                             1991 AGCTTTAGAACGTCTGGAATTTACTGACGAAGAATT 1956
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                                                                                                  535 TICACICAACAACTIGGAGITITICIGACGCCGAGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="LT2"
/db_xref="taxon:602"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Salmonella.
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Location/Qualifiers
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BZ568946 1620 bp DNA linear GSS 17-DEC-2002 pace2-164 8165.y2 pace2-164 Pseudomonas aeruginosa genomic clone pace2-164_8165, genomic survey sequence.
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Spencer, D.H., Raymond, C.K., Smith, E.E., Sime, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Bedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
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Whole-Genome-Sequence variation among multiple isolates of Bedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
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/clone="pacs2-164_2569"
/clone lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library."
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University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
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University of Mashington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Exa: 2066857244
Email: craymond@u.washington.edu
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/strain="2-164"
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                     pacs1-60 4617.x1 pacs1-60 Pseudomonas aeruginosa genomic clone
pacs1-60_4617, genomic survey sequence.
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/clone="pacs1-60 4617"
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Tel: 2062216954
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/strain="1-60"
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Best Local Similarity 51.2
Matches 133; Conservative
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                                                                                                                                                                                                                                             680 GCGGTCATCACAACTGCCACGACGACGTTGATCCAGCGCCACACCTTGGGGGCTGGACAGC 739
                                                                                                                                                                                                                                                                                                                                        740 GGGCGTGACAATGCTGCTGCGCCGAAACCCACCAGGGGAACCAGATCAGGCTTGCCGCG 799
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Pseudomonadaceae, Pseudomonas.
1 (bases 1 to 833)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pacs1-60_5975.x1 pacs1-60 Pseudomonas aeruginosa genomic clone
pacs1-60_5975, genomic survey sequence.
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/clone="pacs1-60"
/clone lib="pacs1-60"
/note="clinical isolate 1-60 Whole genomic shotgun
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Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
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Pred. No. 0.21;
0; Mismatches 104; Indels 0.
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                                               ch 2.1%; Score 48.8; DB 29;
1. Similarity 14.5%; Pred. No. 0.21;
47; Conservative 156; Mismatches 121;
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Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
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Class: shotgun.
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/strain="1-60"
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Contact: Chris K. Raymond
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Best Local Similarity 51.6%;
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Submitted (23-JUJ-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'ELUP) why orghisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Centre Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS017SY 1101 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC BACM37L08 of DrosbAC library from Drosophila melanogaster (fruit
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                         /clone="pacs2-164 8165"
/clone lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
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                                                                                                        /organism="Pseudomonas aeruginosa"
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/db_xref="taxon:7227"
/clone="BACN37108"
/clone=lb="brosBAC"
/plaemid="pBeloBACI1"
/note="end::SP6"
                                                                                                                          /mol_type="genomic DNA"
/strain="2-164"
Fax: 2066857244
Email: craymond@u.washington.edu
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BX393687 Homo sapiens NEUROBLAŠTOMA COT 25-NORMALIZED Homo sapiens CDNA clone CSODC001YG07 5-PRIME, mRNA sequence.
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                            301 ACGCGCCAGCGGCGAAAATCCACCGTCCGGTGTCGCCGTATTGCGCGCCGACGCCGCCGA 860
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Peng Liang Email : fliang@lifetech.com U
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODCOOLADO4QPI.
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Full-length cDNa libraries and normalization
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17.2%; Pred. No. 0.4;
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Defermination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP From the isogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be feated.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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Tal: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoplante, a major partnership french program in plant genomics Unpublished (2003)
                                                   187 TTCGACGAGGCCACGGGCCTTCGAGATCCACCTCGCCGGCACCTGCTACGTCCACTTC
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48.1%; Pred. No. 0.98;
tive 0; Mismatches 140; Indels
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and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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/clone="F1103123"
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                                                                                                          176 GATCAACGCCCAAGGTGCCGGCGATGAACAAAAAGACGTCAGAAATTAAACACACGAGAA 1235
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Contact: Walbot V
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Pred. No. 0.9;
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Tel: 650 723 2227
Fax: 650 725 8221
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Plate: 1117004 row: E colum
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/mol type="mcNA"
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/do xref="taxon:4577"
/clone=lib="ilit - Unigene IV from Maize Genome Project"
/clone="This library represents the unique genes found in
/note="This library represents the unique genes found in
the fourth round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 1091 and 3524. Contigs were assembled using
ZmDBAssembler and 2 representatives from each contig were
selected in
                                                  CA829022 620 bp mRNA linear EST 11-DEC-2002
1114036D07.y2 1114 - Unigene IV from Maize Genome Project Zea mays
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1 (baes 1 to 620)
Walbot, V.
Maize ESTS from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                                                                                                                                                                               Stanford University
855 California Ave, Palo Alto, CA 94304, USA
11 650 723 2227
Fax: 650 725 8221
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llarity 46.0%; Pred. No. 2.5;
Conservative 0; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: walbot@stanford.edu
Plate: 1114036 row: D column: 07.
Location/Qualifiers
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Department of Biological Sciences
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                                                                                       cDNA, mRNA sequence.
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BQ704105 644 bp mRNA linear EST 16-JUL-2002 946110C04.y1 946 - tassel primordium prepared by Schmidt lab Zea
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Maize ESTs from various cDNA libraries sequenced at Stanford
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Tel: 650 723 2227
Fax: 650 725 8221
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to 3 Kb with a 1 Kb average.
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Department of Biological Sciences
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/cultivar="0H43"
/db_xref="taxon:4577"
/tissue_type="tassels"
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Location/Qualifiers
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                                                          mays cDNA, mRNA sequence.
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Search completed: March 16, 2004, 02:52:19

RESULT 15 BQ704105

Job time : 6529.5 secs

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